

Table 121B. Protein Sequence Properties NOV121a	
PSort analysis:	0.6400 probability located in plasma membrane; 0.4600 probability located in Golgi body; 0.3700 probability located in endoplasmic reticulum (membrane); 0.1000 probability located in endoplasmic reticulum (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV121a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 121C.

Table 121C. Geneseq Results for NOV121a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV121a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM78688	Human protein SEQ ID NO 1350 - Homo sapiens, 590 aa. [WO200157190-A2, 09-AUG-2001]	1..572 10..580	388/576 (67%) 449/576 (77%)	0.0
AAM39343	Human polypeptide SEQ ID NO 2488 - Homo sapiens, 589 aa. [WO200153312-A1, 26-JUL-2001]	20..571 37..587	331/555 (59%) 404/555 (72%)	0.0
AAM41129	Human polypeptide SEQ ID NO 6060 - Homo sapiens, 646 aa. [WO200153312-A1, 26-JUL-2001]	20..571 94..644	331/555 (59%) 404/555 (72%)	0.0
AAY39920	Human steroid sulphatase protein sequence - Homo sapiens, 583 aa. [WO9950453-A1, 07-OCT-1999]	20..569 26..575	295/559 (52%) 374/559 (66%)	e-166
AAB51185	Human sulfatase protein C SEQ ID NO:14 - Homo sapiens, 583 aa. [US6153188-A, 28-NOV-2000]	20..569 26..575	294/559 (52%) 372/559 (65%)	e-165

In a BLAST search of public sequence databases, the NOV121a protein was found to have homology to the proteins shown in the BLASTP data in Table 121D.

Table 121D. Public BLASTP Results for NOV121a				
Protein Accession Number	Protein/Organism/Length	NOV121a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P54793	Arylsulfatase F precursor (EC 3.1.6.-) (ASF) - Homo sapiens (Human), 591 aa.	1..572 10..581	379/577 (65%) 441/577 (75%)	0.0
AAH20229	HYPOTHETICAL 64.9 KDA PROTEIN - Homo sapiens (Human), 593 aa.	4..574 24..593	358/574 (62%) 440/574 (76%)	0.0
P51689	Arylsulfatase D precursor (EC 3.1.6.-) (ASD) - Homo sapiens (Human), 593 aa.	4..574 24..593	349/574 (60%) 429/574 (73%)	0.0
P51690	Arylsulfatase E precursor (EC 3.1.6.-) (ASE) - Homo sapiens (Human), 589 aa.	20..571 37..587	334/555 (60%) 405/555 (72%)	0.0
P08842	Steryl-sulfatase precursor (EC 3.1.6.2) (Steroid sulfatase) (Steryl- sulfate sulfohydrolase) (Arylsulfatase C) (ASC) - Homo sapiens (Human), 583 aa.	20..569 26..575	295/559 (52%) 374/559 (66%)	e-166

PFam analysis predicts that the NOV121a protein contains the domains shown in the Table 121E.

Table 121E. Domain Analysis of NOV121a			
Pfam Domain	NOV121a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Sulfatase: domain 1 of 1	21..504	231/530 (44%) 410/530 (77%)	1e-187

Example 122.

The NOV122 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 122A.

Table 122A. NOV122 Sequence Analysis

Table 122A. NOV122 Sequence Analysis			
		SEQ ID NO: 339	3005 bp
NOV122a, CG59746-01 DNA Sequence	<p>ATTTCTTTGGTGTGTGCTTCACAGCTGAACCTGCAAAACAGATTGGAACCTCAAGATIT ATCAATAATCGGAGATACGTATATTTTATTGTAAAGAAAACATGGCTGCCCTATTCC TACGTGGTTTTGTCCAAATAGGGAACCTGCAGACTGGGATATCTAAGTCAAAAGAAAGC ATTCATTGAAGCAGTGGAAAGAAAGACAAAGATAGACATGGTGTGCTTTTCAAAGGT GGAAAATATAGCACTTTTCGGCTAAGTGATAATATTCAAATGTAGTCCCTTAAATCCT ATAGAGGAAACCAAAATCACCTGCATTAACTTTACAAAATAATAATGGCTTGTATTAT TGAAGGATTATCCTCCACAGATGCTGAACAATTGAAGATATTTCTGGACAGAGTTTCAT CAAAAACGAGTTTCAGCCACCTGTGAGACCTGGTAAGGGTGGGAGTGCTTTTCTAGCA CAACACAGAAGGAAATCAACAAAACCTTCATTCCACAAAGTTGATGAGAAATCAAGTAG CAAAATCTTTTGAGATAGCAAAAGGAAGTGGGACAGGTGTCTTCAGAGGATGCCTTTG CTTACATCAAAATTGACACTTACTTGGCGAGAGTTATCAGAAAATCAGCAAGAAGA GGAAAAGAATGCTCTCATCTAGCTCAGAGATGAATGAGGAATTCTTGAAAGAAAATAA TTCTGTAGAATACAGAAATCCAAGGCAGATTGTTTCGAGGTGTGAAGCTATAATCGA GAGAAACAATTGAAGTTAAAAGAGTTAGAAGAGAATAAGAAATTTGGAATTTGAATCTT CATGCATCATGAAGCCCACTGGAAATCCTTACCTAGATGACATTTGGTCTCTCCAAGC TCTCACTGAGAAAATGGTTTTGGTATTCTGTTACAACAAGGGTATAGTGACGGTTAC ACAAAGCTGGGATAAATTTAAACCTATTTTTTGAATTTATTTCCAGAGAAAATATGCCACG GCTCCCAATTTGGGAAACACCTGTTATATGAATGCAGTGTGTACAGTCTCTACTTTTC AATCCCATCGTTTGTGTGATTTACTTAATCAGAGTTTCCCATGGGGTAAAATTTCCC CTTAATGCTCTTACCATGTGCTTGGCACGGCTACTTTTTTTTAAAGATACCTATAATA TAGAAATCAAGGAGATGTTACTCTTGAATCTTAAAAGGCCATTTCCAGCAGCTGCAGA GATATTCATGGCAATGCACAGAACGATGCTCATGAGTTTTTAACTCAGTGTTTAGAT CAACTGAAAGATAACATGGA AAAACCTCAACCAATTTGGAAGCCTAAAAGTGAATTTG GGGAAGATAATTTTCTTAAACAGGTTTTTGTGTGATGATCCTGACACCCAGTGGGTTTTCT TTGCCCTGTCAATTTACTAATTTTGAAGTTAGAGTTGTTGCACTGCATCTGTTGAAGGT TGTGGTCAGGTTATTCTCAAGACAGAACCTGAATAATTACCTCTCCATCAACCTTCCCC AAAGAAATAAAGCACATCCTTCATCTATTCACTCTACTTTTGATCTTTTTTTTGGAGC AGAAGAGCTTGAGTATAAATGTGCAAAATGTGAGCACAAAGATTCGGTTGGAGTGAC TCATTCACTAGGCTTACCTAGAATCCTTATTGTTCACTTCAAAGCGTATAGCTTGAATG AGTTTTGTGCATTAAGAAGAATGACCAAGGAAGTCATCAATTTCCAAATATTAAAGGT GTCTTCTCATTGCAATGAAGGCACCAGACCACCTCTCCCTTGAGTGAGGATGGAGAA ATTACAGATTTCCAATTATTAAGAAGTTATTGAAAGATGACTTCTGGAACAATCATGTG TATCATGGCCTGCAACAAAGGAATCCAAGATATCTGGCTCCACACATTTGGATCAGA TAAGGAGCTCTGAACAAAAAAGGCCAGACAGCTTTTAAAGGGCGAAGCAGAAGACAG CAGCAAAAGTACCTTTGGA AAAAATTTCTAACCAAAATGAGCTAGAATCTGTATCTCAG GAGATCGAGCATTCATTGAAAAAGAACCGTTAGCTCACTTAATGACGTATCTGGAAGA TACCTCACTTTGTGAGTTCCACAAAGCTGGAGGTAACCTGCCAGCAGCCAGGACACA CCTCTCTCAAAGTTGACTTTCAAACAGTGCCCGAAAAATCCAAACGAAAGAAATATG TGAAAACCAAGTAAGTTTGTAGCTTTTGTAGGATTATCAATCTCAATGAAGATTGTGA TGAAGATAAAAAATATCAGAATTCAGAAAGATTCCAAAAAGTGTCTGAACAGACTCAG CAGTGTGACGGTATGAGAATCTGTGAACAAGCCCTCAGCAGGCATGCCTCAAAGCT TTCCAAAGCCAGGCACCCAGGGGCACACAAGAACCTCCTAAGACCTACAAAAATTA TCTACAGAAGTCTAACAGGAATTCCTACTTGCCTGGGTTCCAATAAGAATCCAAGA AACAAAGACATTTTAGATAAGATAAAATCTAAAGCCAAAGGAAACAAAAAGAAATGATG ATAAGGGAGATCATACCTACCGGCTCATTAGTGTGTGACCCATCTTGGGAAGACTCT AAAGTCAGGCCATTATATCTGTGATGCTCATGACTTTGAGAAACAGATCTGTTTCACT TACGATGATATGCGGGTGTAGGTATCCAGGAGGCCAGATGCAGGAGGATAGGCGTT GCACTGGGTACATCTTCTTTTACATGCATAATGAGATCTTTGAAGAGATGTTGAAAAG AGAAGAGAATGCCAGCTTAATAGCAAGGAGGTAGAGGAGACCTTCAGAGGAATAA GAGGAACGTACTCTCTCTGTACAGATCTGCCTGACTGTCTCACTCGATACCCTTCC TCCATGGAAGGAAACCTGTGAACCTTTATCCAGAGATGAAAATGCAATTAGTCTTAGGAC CAAAGGTCAAACAGAAACACTTAATGGGGAGATCGCATTCTAATCC</p>		
	ORF Start: ATG at 101	ORF Stop: TAA at 2840	
	SEQ ID NO: 340	913 aa	MW at 104046.0kD
NOV122a, CG59746-01 Protein Sequence	<p>MAALFLRGFVQIGNCKTGISKSEAFIEAVERKKDRLVLVYFKSGKYSTFRLSQNIQN VVLKSYRGNQNLHLTLQNNNGLFIEGLSSDQAEQLKIFLDRVHQNEVQPPVRPGKGG SVFSSTTQKEINKTSFHKVDEKSSSKSFEIAKSGSGTVLQRMPLLTSLKLTLCBELSE NQHKRKRMLSSSSSEMNEEFLEKNNNSVEYKSKFADCSRCSVSNREKQLKLKELENNK LECESSICMNATGNPYLDDIGLLQALTEKMYLVFLQQGYSDGYTKWKLKLFELFP LLECHNPNLNTTMMWVWVQALDISEAFDILNLPWVWYDNLALTMALRLEP</p>		

KRKKYVKTSEFVAFDRIINPTKDLYEDKNIRIPERFQKVSEQTQQCDGMRICEQAPOQ ALPQSFPPKPGTQGHKTNLLRPTKLNQKSNRNSLLALGSNKNPRNKDILDKIKSKAKE TKRNDKGDHTYRLISVSHLGKTLKSGHYICDAYDFEKQIWFTYDDMRVLGIQEAQM QEDRRTGYIFFYMHNEIFEMLKREENAQLNSKEVEETLQKE

Further analysis of the NOV122a protein yielded the following properties shown in Table 122B.

Table 122B. Protein Sequence Properties NOV122a	
PSort analysis:	0.7000 probability located in nucleus; 0.4270 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.1047 probability located in mitochondrial inner membrane
SignalP analysis:	Likely cleavage site between residues 16 and 17

A search of the NOV122a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 122C.

Table 122C. Geneseq Results for NOV122a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV122a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU07888	Polypeptide sequence for human hspG25 - Homo sapiens, 913 aa. [WO200166752-A2, 13-SEP-2001]	1..913 1..913	913/913 (100%) 913/913 (100%)	0.0
AAB75607	Human cancer associated antigen precursor HOM-TES-84/6 SEQ ID NO:6 - Homo sapiens, 912 aa. [WO200100874-A2, 04-JAN-2001]	1..905 1..904	429/920 (46%) 566/920 (60%)	0.0
AAU07869	Polypeptide sequence for mammalian SpG25 - Mammalia, 835 aa. [WO200166752-A2, 13-SEP-2001]	1..904 1..834	335/921 (36%) 504/921 (54%)	e-147
AAG75460	Human colon cancer antigen protein SEQ ID NO:6224 - Homo sapiens, 109 aa. [WO200122920-A2, 05-APR-2001]	810..912 3..107	61/105 (58%) 79/105 (75%)	3e-28
AAB39364	Gene 8 human secreted protein homologous amino acid sequence	810..871 1..64	39/64 (60%) 48/64 (74%)	5e-15

In a BLAST search of public sequence databases, the NOV122a protein was found to have homology to the proteins shown in the BLASTP data in Table 122D.

Table 122D. Public BLASTP Results for NOV122a				
Protein Accession Number	Protein/Organism/Length	NOV122a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9BXU7	Ubiquitin carboxyl-terminal hydrolase 26 (EC 3.1.2.15) (Ubiquitin thiolesterase 26) (Ubiquitin-specific processing protease 26) (Deubiquitinating enzyme 26) - Homo sapiens (Human), 913 aa.	1..913 1..913	913/913 (100%) 913/913 (100%)	0.0
Q9HBJ7	UBIQUITIN-SPECIFIC PROCESSING PROTEASE - Homo sapiens (Human), 922 aa.	1..905 1..904	429/920 (46%) 566/920 (60%)	0.0
Q9HCH8	KIAA1594 PROTEIN - Homo sapiens (Human), 931 aa (fragment).	50..912 3..929	393/932 (42%) 535/932 (57%)	e-171
Q99MX1	Ubiquitin carboxyl-terminal hydrolase 26 (EC 3.1.2.15) (Ubiquitin thiolesterase 26) (Ubiquitin-specific processing protease 26) (Deubiquitinating enzyme 26) - Mus musculus (Mouse), 835 aa.	1..904 1..834	335/921 (36%) 504/921 (54%)	e-147
Q9ES63	UBIQUITIN-SPECIFIC PROCESSING PROTEASE - Mus musculus (Mouse), 869 aa.	1..908 1..848	341/933 (36%) 480/933 (50%)	e-131

PFam analysis predicts that the NOV122a protein contains the domains shown in the Table 122E.

Table 122E. Domain Analysis of NOV122a			
Pfam Domain	NOV122a Match Region	Identities/ Similarities for the Matched Region	Expect Value
UCH-1: domain 1 of 1	295..326	21/32 (66%) 29/32 (91%)	8.8e-12

Example 123.

The NOV123 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 123A.

Table 123A. NOV123 Sequence Analysis			
	SEQ ID NO: 341	2146 bp	
NOV123a, CG88613-01 DNA Sequence	GAAGGAGCGGGCATGAGGCGCTGCCGTGCCGTGGGAGCCTGAACGAGGCGGAGGCCG GGGCGCTGCCCGCGGCGGCCCGCATGGGACTGGAGGCGCGCGAGGAGGGCGGCGCGG GCAGCCGGGACAGCAGCGACCTGGGCCCGCGCAGGGGCCCCGCGGGCGGCGCGGAG GGGGGCGGGCCCTGGGCCCGGACAGAGGGTCCAGCCTCCAGAGCGAGCCTGAGAGGG CCGGCCTCGGGCCTGGCCCGGGACAGAGAGTCCGAGGCAGAAATTCGGACAGACGG ACAGACTGAGCCCGCGGCAGCTGGCCTTGGAGTAGAGACCGAGAGGCCCAAGCAAAAG ACGGAGCCAGACAGGTCCAGCCTCCGGACGCATCTAGAATGGAGCTGGTCAGAGCTGG AGACGACTTGTCTTTGGACGGAGACCGGGACAGATGGCCTTTGGACTGATCCGCACAG GTCCGACCTCCAGTTTCAGCCCGAGGAGGCCAGCCCCCTGGACACAGCCAGGGGTTCA GGGCCCTTGACACAGCTGGAACCGCATGGGTACAGACTCAGCCAGAGAGGGTCAAGT CCTGGGCTGATAACCTCTGGACCCACCAGAACAGTTCCAGCCTCCAGACTCACCAGA AGGAGCCTGTCCCTCAAAAGAGCCAAAGTGCTGATGGCTCCTGGAAAGAATTGTATACT GATGGCTCCAGGACACAACAGGATATTGAAGGTCCCTGGACAGAGCCATATACTGATG GCTCCCAAGAAAAACAGGATACTGAAGCAGCCAGGAAACAGCCTGGCACTGGTGGTTT CCAAATACAACAGGATACTGATGGCTCCTGGACACAACCTAGCACTGACGGTTCCAG ACAGCACCTGGGACAGACTGCCTCTTGGGAGAGCCTGAGGATGGCCATTAGAGGAAC CAGAGCCTGGAGAATTGCTGACTCACCTGTACTCTCACCTGAAGTGTAGCCCCCTGTG CCCTGTGCCCCGCTCATCATTACCCCTGAGACCCCTGAGCCTGAGGCCAGCCAGTG GGACCCCTCCCGGGTTGAGGGGGGCAGCGCGGCTTCTCCTCTGCTCTTCTTCG ACGAGTCTGAGGATGACGTGGTGGCCGGGGCGGAGGTGCCAGCGATCCCGAGGACAG GTCTGGGAGCAAAACCTGGAAGAAGCTGAAGACAGTTCTGAAGTATTACCCCTTTGTG GTCTCCTTCCGAAAACACTACCCTTGGGTCCAGCTTCTTGACATGTCTGGAACTTCC AGGCAGGAGAGGATGGTGGATTCTGAAACGTTTCTGTGAGTGTAGCAGCGCAGCCT GGAGCAGCTGATGAAAGACCCGCTGCGACCTTTCGTGCTGCTGCTACTATGGCATGGTG CTGCAGGATGGCCAGACCTTCAACCAGATGGAAGACCTCCTGGCTGACTTTGAGGGCC CCTCCATTATGGACTGCAAGATGGGCAGCAGGACCTATCTGGAAGAGGAGCTAGTGAA GGCACGGGAACGTCCCGTCCCGGAAGGACATGTATGAGAAGATGGTGGCTGTGGAC CCTGGGGCCCTACCCCTGAGGAGCATGCCCAGGGTGCAGTACCAAGCCCGCTACA TGCAGTGGAGGGAACCATGAGCTCCACCTCTACCCTGGGCTTCCGGATCGAGGACAT CAAGAAGGCAGATGGGACCTGTAACACCACTTCAAGAAGACGCGGACCTGGAGCAG GTGACAAAAGTGTGGAGGACTTCGTGGATGGAGACCAGTCACTCCTGCAAAAGTACG TGGCATGCCTAGAAGAACTTCGTGAAGCTCTGGAGATCTCCCCCTTCTTCAAGACCCA CGAGGTGGTAGGCAGCTCCCTCCTCTTCGTGCACGACCACACCGGCTGGCCAAAGTCT TGGATGATAGACTTCGGCAAGACGGTGGCCTTGCCCGACCACCAGACGCTCAGCCACA GGCTGCCCTGGGCTGAGGGCAACCGTGAGGACGGCTACCTCTGGGGCTGGACAACAT GATCTGCCTCCTGCAGGGGCTGGCACAGAGCTGAGCTGCTCAGCCACCATCAGGTTAA TTGGATGGGCCAGTCTGGCTGGAGGAGCCCTGAGATGCCATGGGAGGCGCTGAGGTTG		
	ORF Start: ATG at 13	ORF Stop: TGA at 2062	
	SEQ ID NO: 342	683 aa	MW at 75206.8kD
NOV123a, CG88613-01 Protein Sequence	MRRCPGRGSLNEAEAGALPAAARMGLEAPRGRRRQPGQQRPGPGAGAPAGRPEGGGP WARTEGSSLSHSEPERAGLGAPGTESPAEFWTDGQTEPAAAGLGVETERPKQKTEPD RSSLRTHLEWSWSELETTCLWTETGTDGLWTDPHRSDLQFQPEEASPTQPGVHGPWT ELETHGSGTQPERVKSADNLWTHQNSSSLQTHPEGACPSKEPSADGSKWELYTDGSR TQQDIEGPWTEPYTDGSGKKQDTEAARKQPGTGGFQIQDQTDGWSWTQSTDGSGTAPG TDCLLGEPEPDGPLEFPEPSELLTHLYSHLKCSPLCPVPRLLITPETPEPEAQPVGPPS RVEGSGGFFSSASSFDESEDDVVGAGGGASDPEDRSGSKPKWKLKTVLKYSFVVSFR KHYPKVQLSGHAGNFQAGEDGRILKRFCQCEQRSLEQLMKDPLRFPVAYYGMVLQDG QTFNQMEDLLADFEGPSIMDKMGSRTYLEEELVKARERPRPRKDMYKMWAVDPGAP TPEEHAQGAUTKPRYMQRWRETMSSTSLGFRLEGIKKADGTCNTNFKKTQALEQVTKV LEDFVDGDHVLQKYVACLEELREALEISPFKTHEVVGSSLLFVHDHTGLAKVWMD FGKTVALPDHQTLSHRLPWAEGNREDGYLWGLDNMICLLQGLAQS		

Each amino acid of the NOV123a protein yielded the following properties shown in

Table 123B. Protein Sequence Properties NOV123a	
PSort analysis:	0.5663 probability located in microbody (peroxisome); 0.3000 probability located in nucleus; 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV123a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 123C.

Table 123C. Geneseq Results for NOV123a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV123a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM41393	Human polypeptide SEQ ID NO 6324 - Homo sapiens, 687 aa. [WO200153312-A1, 26-JUL-2001]	1..683 5..687	682/683 (99%) 682/683 (99%)	0.0
AAM39607	Human polypeptide SEQ ID NO 2752 - Homo sapiens, 711 aa. [WO200153312-A1, 26-JUL-2001]	12..683 36..711	642/680 (94%) 643/680 (94%)	0.0
AAE04364	Human kinase (PKIN)-5 - Homo sapiens, 798 aa. [WO200146397-A2, 28-JUN-2001]	273..682 380..793	219/432 (50%) 285/432 (65%)	e-117

In a BLAST search of public sequence databases, the NOV123a protein was found to have homology to the proteins shown in the BLASTP data in Table 123D.

Table 123D. Public BLASTP Results for NOV123a				
Protein Accession Number	Protein/Organism/Length	NOV123a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96DU7	INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE C -	1..683 1..683	683/683 (100%) 683/683 (100%)	0.0
Q954	INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE C -	1..683 4..604	683/683 (100%) 601/601 (100%)	0.0

	ISOENZYME (EC 2.7.1.127) - Homo sapiens (Human), 604 aa (fragment).			
S17682	1D-myo-inositol-trisphosphate 3-kinase (EC 2.7.1.127) B - human, 472 aa.	273..682 54..467	219/432 (50%) 285/432 (65%)	e-117
CAB65055	INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE B - Homo sapiens (Human), 946 aa.	273..682 528..941	219/432 (50%) 285/432 (65%)	e-117
Q96JS1	INOSITOL 1,4,5-TRISPHOSPHATE 3-KINASE, ISOFORM B (EC 2.7.1.127) - Homo sapiens (Human), 946 aa.	273..682 528..941	219/432 (50%) 285/432 (65%)	e-117

PFam analysis predicts that the NOV123a protein contains the domains shown in the Table 123E.

Table 123E. Domain Analysis of NOV123a

Table 123E. Domain Analysis of NOV123a			
Pfam Domain	NOV123a Match Region	Identities/ Similarities for the Matched Region	Expect Value
No Significant Matches Found			

Example 124.

The NOV124 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 124A.

Table 124A. NOV124 Sequence Analysis

Table 124A. NOV124 Sequence Analysis		
	SEQ ID NO: 343	1395 bp
NOV124a, CG59993-01 DNA Sequence	GGTAAGACGACCTCTGGATGCTCACCCCTGCCCTCTTACCTCTCGTCCCCAGCTGTTT CCTCTGTCACCATGAGGAACATTTTCAAGAGGAACACGAGGCTATTGTGGGCTCCTGC CACCACACCGCCACGATGCCCATTTGACCCCGTGGATCAACTCCACTGAGATGGGGGGT GCTGGGAGAGCCAGGAGGACATGTTGCCAACTGAAGGAGAAGTTATTCAATGAGA TAAACAAGATTCCCTTACCACCCCTGGGCACTGATCGCATGTGCTGSGTTCTGGGGCT CCTGCTTCTACCTGTGCTTCTGTCATCTGCAAGAAATGCTGCTCAAGAAGAAGAAG AACAAGAAGGAGAAGGGCAAGGCATGAAGAAATGCCATGAAGCATGAAGGATGAAG GGGGTGAGGATGACGACGACGACGACGACGAGGCTGATGAGGGGGAAGGTGAAGGGGA GGAGGAGAAAGAGCCAGAGAACTGGGCAAACTGCAGTTTCCCTGGACTATGATTTT CAGGCTAATCAGCTTACTGTGGGCGTTCTGCAGGCTGCTGAACCTGCCTGCCCTGGACA TGGGAGGCACCTCAGACCCTTATGTCAAGGCTCTCCTCCTTCCCTGACAAGAAGAAGAA ATATGAGACCAAAGTCCATCGGAAGACACTGAACCTGCCTTCAATGAAACCTTCACC TTCAAGGTGCCATACCAAGGAGCTTGGGGGCAAACTCTGGTGATGGCCATCTATGACT TTGACCGCTTCTCCAACATGACATCATTGGAGAGGTAAGGTGCCATGAAACACAGT GGACCTCGGGCCAGCCCATTTGAGGAGTGGAGAGACCTGCAAGGGGGGAAAAAGGAGAG	

	ACTCGCTCAAGCCTGAGGAGGAGGTGGATGCACTCCTGGGCAAGAACAAGTAGACAGC AGCGGCTGGGACCCACACCTTTACGGGACACTGACAAGATCCAGAGCTATCAATACC TCA		
	ORF Start: ATG at 70		ORF Stop: TAG at 1327
	SEQ ID NO: 344	419 aa	MW at 46871.8kD
NOV124a, CG59993-01 Protein Sequence	MRNIFKRNQEPVAPATTTATMPIGPVDNSTESGGAGESQEDMFAKLKEKLFNEINKI PLPPWALIAIAVVAGLLLLTCCFCICKKCCCKKKKKKKEKKGKMKNAMNMKDMKGGQD DDDAETGLTEGEGEGEEKEPENLGLQFSLDYDFQANQLTVGVLQAAELPALDMGGT SDPYVKVFLLPDKKKKYETKVHRKTLNPAFNETFTFKVPYQELGGKTLVMAIYDFDRF SKHDIIGEVKVPMTVDLGQPIEWRDLQGGEEKKEPEKLGDICTSLRYVPTAGKLTVC ILEAKNLKKMDVGLSDPYVKIHLMQNGKRLKKKTTVKKKTLNPFYNESFSFEIPFE QIQKVQVVTVLDYDKLGKNEAIGKIFVGSNATGTEL RHWSMDLANPRRPIAQWHS LK PEEEVDALLGKNK		
	SEQ ID NO: 345	1338 bp	
NOV124b, CG59993-02 DNA Sequence	CCACCATGAGGAACATTTTCAAGAGGAACCAGGAGCCTATTGTGGCTCCTGCCACCAC CACCGCCACGATGCCCATTTGGACCCGTGGACAACCTCCACTGAGAGTGGGGGTGCTGGG GAGAGTCAGGAGGACATGTTTGCCTAACTGAAGGAGAAGTTATTCAATGAGATAAACA AGATTCCCTTACCACCTGGGCACTGATCGCCATTGCTGTGGTGTGCTGGGCTCCTGCT TCTCACCTGCTGCTTCTGCATCTGCAAGAAATGCTGCTGCAAGAAGAAGAAGAACAAG AAGGAGAAGGGCAAAGGTATGAAGAATGCCATGAACATGAAGGACATGAAGGGGGT AGGATGACGACGACGAGAGACAGGCTGACTGAGGGGGAAGGTGAAGGGGAGGAGGA GAAAGAGCCAGAGAACCTGGGCAAACCTGCAGTTTTCCCTGGACTATGATTTTACAGCT AATCAGCTTACTGTGGGCGTCTGCAAGGCTGCTGAACCTGCCTGCCCTGGACATGGGAG GCACCTCAGACCCCTATGTCAAGGCTTCTCTCTCTCTGACAAGAAGAAGAATAATGA GACCAAAGTCCATCGGAAGACACTGAACCTGCCTTCAATGAAACCTTACCTTCAAG GTGCCATACCAGGAGCTTGGGGGCAAACTCTGGTGATGGCCATCTATGACTTTGACC GCTTCTCCAACATGACATCATTTGGAGAGGTAAAGGTGCCTATGAACACACTGGACCT CGGCCAGCCCATGAGGAGTGGAGAGACCTGCAAGGCGGGGAAAGAGGAGGCGGAG AAGCTGGGCGACATCTGCACCTCCCTGCGCTATGTGCCACGCGCGGAAGCTCACTG TCTGCATCTCGGAGGCTAAGAACCTCAAGAAGATGGACGTGGGCGGCTTTAGACCC GTACGTGAAGATCCACCTGATGCAGAATGGCAAGAGGCTCAAGAAGAAGAAGACAACC ATGAAGAAGAAGACCTGAACCCATACTTCAACGAGTCCTTACGCTTTGAGATCCCCT TCGAGCAGATTCAAGAAAGTCCAGGTAGTGGTCACCGTGCTGGACTATGACAAGCTGGG CAAGAACGAAGCCATAGGCAAGATCTTCTGTGGGCAGCAATGCCACGGGCGACAGAGCTG CGGCACTGGTCCGACATGCTGGCCAACCCCGGAGGCCCATCGCCAGTGGCACTGCG TCAAGCCTGAGGAGGAGGTGGGTGCACTCCTGGGCAAGACAAGTAGACAGCAGCGGC TGGGACCCACACCTTTACCGGACACTGACAAGATCCAGAGCTATCAATAAGGTGTAG GCGG		
	ORF Start: ATG at 6		ORF Stop: TAG at 1263
	SEQ ID NO: 346	419 aa	MW at 46845.9kD
NOV124b, CG59993-02 Protein Sequence	MRNIFKRNQEPVAPATTTATMPIGPVDNSTESGGAGESQEDMFAKLKEKLFNEINKI PLPPWALIAIAVVAGLLLLTCCFCICKKCCCKKKKKKKEKKGKMKNAMNMKDMKGGQD DDDAETGLTEGEGEGEEKEPENLGLQFSLDYDFQANQLTVGVLQAAELPALDMGGT SDPYVKVFLLPDKKKKYETKVHRKTLNPAFNETFTFKVPYQELGGKTLVMAIYDFDRF SKHDIIGEVKVPMTVDLGQPIEWRDLQGGEEKKEPEKLGDICTSLRYVPTAGKLTVC ILEAKNLKKMDVGLSDPYVKIHLMQNGKRLKKKTTMKKTLNPFYNESFSFEIPFE QIQKVQVVTVLDYDKLGKNEAIGKIFVGSNATGTEL RHWSMDLANPRRPIAQWHS LK PEEEVGALLGKNK		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 124B.

Table 124B. Comparison of NOV124a against NOV124b.		
Protein Sequence	NOV124a Residues/ Match Residues	Identities/ Similarities for the Matched Region

Further analysis of the NOV124a protein yielded the following properties shown in Table 124C.

Table 124C. Protein Sequence Properties NOV124a	
PSort analysis:	0.8202 probability located in mitochondrial inner membrane; 0.6000 probability located in endoplasmic reticulum (membrane); 0.3500 probability located in nucleus; 0.3034 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV124a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 124D.

Table 124D. Geneseq Results for NOV124a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV124a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAR97722	Mouse inositol polyphosphate binding protein IP4-BP - Mus musculus, 422 aa. [JP08092290-A, 09-APR-1996]	1..419 1..422	412/422 (97%) 414/422 (97%)	0.0
AAU19715	Human novel extracellular matrix protein, Seq ID No 365 - Homo sapiens, 461 aa. [WO200155368-A1, 02-AUG-2001]	128..405 169..447	141/280 (50%) 201/280 (71%)	2e-80
AAU19714	Human novel extracellular matrix protein, Seq ID No 364 - Homo sapiens, 295 aa. [WO200155368-A1, 02-AUG-2001]	141..409 11..281	140/273 (51%) 193/273 (70%)	3e-74
AAW87702	A human membrane fusion protein designated SYNTAX2 - Homo sapiens, 375 aa. [WO9856813-A2, 17-DEC-1998]	59..407 31..364	146/352 (41%) 220/352 (62%)	4e-73
AAO05534	Human polypeptide SEQ ID NO 19426 - Homo sapiens, 149 aa.	33..164 15..149	127/135 (94%) 131/135 (96%)	5e-70

BLASTP SEARCH OF PUBLIC SEQUENCE DATABASES: THE NOV124a PROTEIN WAS FOUND TO HAVE HOMOLOGY TO THE PROTEINS SHOWN IN THE BLASTP DATA IN TABLE 124E.

Table 124E. Public BLASTP Results for NOV124a				
Protein Accession Number	Protein/Organism/Length	NOV124a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
P29101	Synaptotagmin II (SytII) - Rattus norvegicus (Rat), 422 aa.	1..419 1..422	411/422 (97%) 414/422 (97%)	0.0
A55417	synaptotagmin II - mouse, 422 aa.	1..419 1..422	412/422 (97%) 414/422 (97%)	0.0
P46097	Synaptotagmin II (SytII) - Mus musculus (Mouse), 422 aa.	1..419 1..422	411/422 (97%) 413/422 (97%)	0.0
P24506	Synaptotagmin B (Synaptic vesicle protein O-P65-B) - Discopyge ommata (Electric ray), 439 aa.	10..419 27..439	341/413 (82%) 366/413 (88%)	0.0
P46096	Synaptotagmin I (SytI) (p65) - Mus musculus (Mouse), 421 aa.	10..419 8..421	323/418 (77%) 353/418 (84%)	0.0

PFam analysis predicts that the NOV124a protein contains the domains shown in the Table 124F.

Table 124F. Domain Analysis of NOV124a			
Pfam Domain	NOV124a Match Region	Identities/ Similarities for the Matched Region	Expect Value
Adeno_E3_CR2: domain 1 of 1	62..108	16/50 (32%) 26/50 (52%)	6.5
C2: domain 1 of 2	156..242	54/97 (56%) 81/97 (84%)	1.8e-42
C2: domain 2 of 2	287..375	44/97 (45%) 80/97 (82%)	2.9e-39

Example 125.

The NOV125 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 125A.

Table 125A. NOV125 Sequence Analysis

SEQ ID NO: 347	3226 bp
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NOV125a, CG59991-01 DNA Sequence	GGACCACTTCTGATGCATCTCTGGGTCCCAACTATCCACTGCAAGGCCTCGAAACA GGGGGGCCAGATGGGACCCCATTTAGCACAAGAGAGAGCTCCACTCTGTGAGCCC AAAGGGAGAGGGCTCAGGCCACGGCAGAGAGCGGAACAGGAAACCGTCACGAAAAACA GCCTCAAGTGGCAGGTCCCTTGCAGGAACAGACAGGCCTGGGGCCGCCCCACCTGGG CTCAGAGCTTGGGTGTCATGGAGGTGACACATGGGACTACAAGAGTCACGTGATGACC AAATTCGCTGAGGAGGAGGATGTACGTCTGTAGTTTGAACAACTGGTGTGACTGGC CGGAAATGCAACGTTGGCTGGTGCTTTTGATTGACACCGTGGGGCTTCCGGCTCG CACGGTGGTTCTGCACGAAAGTCAGGAATTGGGAAATCGGCTCTAGCCAGAAGGATC GTGCTGTGCTGGGCGCAAGGTGGACTCTACCAGGGAATGTTCTCTACGTCTTCTTCC TCCCCGTTAGAGAGATGCAGCGGAAGAAGGAGAGCASTGTACAGAGCTTCATCTCCAG GGAGTGGCCAGACTCCAGGCTCCGGTGACGGAGATCATGTCCCGACCAGAAAGGCTG TTGTTTCATCATTGACGGTTTCGATGACCTGGGCTCTGTCTCAACAATGACACAAAGC TCTGCAAGACTGGGCTGAGAAGCAGCCTCCGTTACCCCTCATACGAGTCTGTGAG GAAGGTCTGTCTCCGTGAGTCTTCTGATCGTCACCGTCAGAGCTGGGCACAGAG AAGCTCAAGTCAGAGGTGCTGTCTCCCGTTACCTGTTAGTTAGAGGAATCTCCGGGG AACAAGAAATCCACTTGCTCTTGAAGCGGGATTGGTGAGCATCAGAAGACACAAG GTTGCGTGGATCATGAACAACCGTGAGCTGCTCGACCAAGTGCAGGTCGCGCGCTG GGCTCTCTCATCTGCGTGGCCCTGCAGCTGCAGGAGCTGGTGGGGGAGAGCGTCGCCC CCTTCAACCAACGCTCACAGGCTGCACGCCGCTTTTGTGTTTCATCAGTCAACCCC TCGAGGCGTGGTCCGGCGCTGTCTCAATCTGGAGGAAAGAGTTGTCTGAAGCGCTTC TGCCGTATGGCTGTGGAGGGAGTGTGGAATAGGAAGTCAGTGTTCGCGTACGAGC TCATGGTTCAAGGACTCGGGAGTCTGAGTCCGTGCTCTGTTTCATATGAACATCCT TCTCCAGACAGCACTGTGAGGAGTACTACACCTTCTTCCACCTCAGTCTCCAGGAC TCTGTGCGCGCTTGTAACGTGTAGAGGGCTGGAAATCGAGCCAGCTCTCTGTC CTCTGTACGTTGAGAAGACAAGAGGTCCATGGAGCTTAAACAGGCAGGCTTCCATAT CCACTCGCTTGGATGAAGCGTTTCTGTGTTGGCTCGTGAGCGAAGACGTAAGGAGG CCACTGGAGGTCTGTGGGTGTCCCGTTCCCTGGGGGTGAAGCAGAAGCTTCTGC ACTGGGTCTCTGTGTTGGGTGAGGAGCTTAATGCCACCCAGGAGGACACCTTGGGA CGCCTTCCACTGTCTTTTCGAGACTCAAGACAAGAGTTGTTGCTGTGGCATTAAAC AGCTTCCAAGAAAGTGTGGCTTCCGATTAACAGAACCTGGACTTGATAGCATCTTCCT TCTGCTCCAGCACTGTCCGTATTGCGGAAATTCGGGTGGATGTCAAAGGATCTT CCCAAGAGATGAGTCCGCTGAGGCATGTCTGTGGTCCCTCTATGGATGCGGGATAAG ACCCTCATGAGGAGCAGTGGGAAGATTTCTGCTCCATGCTTGGCACCACCCACACC TGCGGCAGCTGGACCTGGGCAGCAGCATCTGACAGAGCGGGCCATGAAGACCCCTGTG TGCCAAAGCTGAGGCATCCACCTGCAAGATACAGACCCCTGATGTTTAGAAATGCAAG ATTACCCCTGGTGTGCAGCACCTCTGGAGAATCGTCATGGCCAACCGTAACCTAAGAT CCCTCAACTTGGGAGGCACCCACCTGAAGGAAGAGGATGTAAGGATGGCGTGTGAAGC CTTAAACACCCAAATGTTTGTGGAGTCTTGGAGCTGGATTGCTGTGGATTGACC CATGCTGTTTACCTGAAGATCTCCCAAATCCTTACGACCTCCCCAGCCTGAAATCTC TGAGCCTGGCAGGAACAAGGTGACAGACCAGGGAGTAATGCTCTCAGTGTGCTT GAGAGTCTCCAGTGCGCCCTGCAGAAGCTGATACTGGAGGACTGTGGCATCACAGCC ACGGGTGGCAGAGTCTGGCTCAGCCCTCGTCAGCAACCGGAGCTGTGACACAGCTGT GCCTATCCAACAACAGCCTGGGAACGAAGGTGTAATCTACTGTGTCGATCCATGAG GCTTCCCCACTGTAGTCTGCAGAGGCTGATGCTGAATCAGTGGCACCCTGGACAGGCT GGCTGTGGTTTCTTGCCTTATGGGTAATCATGGTGTGACGCACCTGAGCC TTAGCATGAACCCCTGTGGAAGACAATGGCGTGAAGCTTCTGTGCGAGGTCATGAGAGA ACCATTTGTCTATCTCCAGGACTGGAGTTGGTAAAGTGTATCTACCGCGCGCTGTC TGTGAGAGTCTGTCTGTGTGATCTCGAGGAGCAGACACCTGAAGAGCCTGGATCTCA CGGACAATGCCCTGGGTGACGGTGGGTTGCTGCCTGTGCGAGGAGTGAAGCAAAA GAACAGTGTCTGACGAGACTCGGGTTGAAGGCATGTGGACTGACTTCTGATGTCTGT GAGGCACTCTCTTGGCCCTTTCTCTGCAACCGGCATCTGACCACTTAAACCTGGTGC AGAATAACTTCAGTCCCAAAGGAATGATGAAGCTGTGTTCCGCTTGGCCTTCCAC GTCTAACTTACAGATAATTGGGCTGTGGAATGGCAGTACCCTGTGCAAAATGAAGAG CTGCTGGAGGAAGTGCAGTACTCAAGCCCCGAGTGTGTAATTGACGGTAGTTGGCATT CTTTTGATGAAGATGACCGGTACTGGTGGAAAACTGAAGATACGGAACCTGCCCCA CTCACCCCATCTGATGGAGGAACCTTAAACGCTGT
	ORF Start: ATG at 69 ORF Stop: TGA at 3168
	SEQ ID NO: 348 1033 aa MW at 116310.7kD
NOV125a, CG59991-01 Protein Sequence	MGPPFSTRETSLCEPKGRRLRPRQRNQNENVTNLSKLPGPLQEQTGLGPPHLSSEL GLHGGDTWDYKSHVMTKFAEEDVRRSFENTAADWPEMQTLAGAFDSRWGFRPRTVV LHGKSGIGKSALARIVLCWAQGLYQGMFSYVFFLPVREMQRKKESVTEFISREWP DSQAPVTEIMSRPERLLFIIDGFDLLGSLVNLNDTKLCKDWAEEKQPPFTLIRSLRKLVL LPESFLIVTVRDVGTETKLKSEVVSPLYLLVRGTSGEQRIHLLRERGIGEHQTLQGLRA IMNRELLDQCQVPVAVSLICVALQLQDVVGESVAFNQTLTLGLHAAFVHQLTFRGV VRRCLNLEERVVLKRCFRMAVEGVVNRKSVFDGDDLMVQGLGESELRLALFHMNILLPD SHCEEYTFHLSLQDFCAALYVLEGLEIEPALCPLYVEKTKRSMELKQAGFHLSL WMKRFLEGLNSEDVPPPLFVLLGCPVPIGVFQKLLHWVSLLGQPNATTGGDTLDAFH

	LTRIGLGLKACGLTSDCCEALSLALSCNRHLTSLNLVQNNFSPKGMMLCSAFACPTSNL QIIGLWKWQYPVQIRKLLLEEVQLLKPRVVIDGSWHSFDEDDRYWWKN
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Further analysis of the NOV125a protein yielded the following properties shown in Table 125B.

Table 125B. Protein Sequence Properties NOV125a	
PSort analysis:	0.7600 probability located in nucleus; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV125a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 125C.

Table 125C. Geneseq Results for NOV125a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV125a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAE07514	Human PYRIN-1 protein - Homo sapiens, 1034 aa. [WO200161005-A2, 23-AUG-2001]	103..934 207..1003	276/843 (32%) 445/843 (52%)	e-126
AAE07513	Human nucleotide binding site 1 (NBS-1) protein - Homo sapiens, 1033 aa. [WO200161005-A2, 23-AUG-2001]	114..935 180..990	281/839 (33%) 431/839 (50%)	e-120
AAU07878	Polypeptide sequence for mammalian Spg65 - Mammalia, 748 aa. [WO200166752-A2, 13-SEP-2001]	207..963 9..748	218/766 (28%) 380/766 (49%)	7e-95
AAE06758	Human G-protein coupled receptor-8 (GCREC-8) protein - Homo sapiens, 1473 aa. [WO200157085-A2, 09-AUG-2001]	21..764 219..959	235/772 (30%) 380/772 (48%)	3e-88
AAB62571	Human CARD-7 polypeptide - Homo	21..764	235/772 (30%)	3e-88

In a BLAST search of public sequence databases, the NOV125a protein was found to have homology to the proteins shown in the BLASTP data in Table 125D.

Table 125D. Public BLASTP Results for NOV125a				
Protein Accession Number	Protein/Organism/Length	NOV125a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q9JLR2	MATERNAL-ANTIGEN-THAT-EMBRYOS-REQUIRE PROTEIN - Mus musculus (Mouse), 1111 aa.	24..1033 104..1111	548/1019 (53%) 716/1019 (69%)	0.0
Q9R1M5	MATER PROTEIN - Mus musculus (Mouse), 1111 aa.	24..1033 104..1111	547/1019 (53%) 716/1019 (69%)	0.0
AAL35293	NALP4 - Homo sapiens (Human), 994 aa.	63..958 94..981	291/907 (32%) 473/907 (52%)	e-133
Q96MN2	CDNA FLJ32126 FIS, CLONE PEBLM2000112, WEAKLY SIMILAR TO HOMO SAPIENS NUCLEOTIDE-BINDING SITE PROTEIN 1 MRNA - Homo sapiens (Human), 919 aa.	63..958 19..906	291/907 (32%) 473/907 (52%)	e-133
AAL12497	CRYOPYRIN - Homo sapiens (Human), 1034 aa.	103..934 207..1003	276/843 (32%) 445/843 (52%)	e-125

PFam analysis predicts that the NOV125a protein contains the domains shown in the Table 125E.

Table 125E. Domain Analysis of NOV125a			
Pfam Domain	NOV125a Match Region	Identities/ Similarities for the Matched Region	Expect Value
LRR: domain 1 of 6	671..695	6/25 (24%) 16/25 (64%)	1.6e+02
LRR: domain 2 of 6	728..752	7/27 (26%) 17/27 (63%)	2.3e+02
LRR: domain 4 of 6	814..836		4.5e+02

		14/25 (56%)	
LRR: domain 5 of 6	899..923	8/26 (31%) 20/26 (77%)	27
LRR: domain 6 of 6	956..977	7/25 (28%) 16/25 (64%)	2.9e+02

Example 126.

The NOV126 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 126A.

Table 126A. NOV126 Sequence Analysis

[illegible]

	EGDLGFTLRGNAPVQVHFLDPYCSASVAGAREGDYIVSIQLVDCWKWLTLSFVMKLLKS FGEDEIEMKVVSLLDSTSSMHNKSATYSVGMQKTYSMICLAIDDDDKTDKTKKISKLL SFLSWGINKNRQSASTLCLPSVGAARPQVKKKLPSFPFLLNSDSSWY		
	SEQ ID NO: 351	2109 bp	
NOV126b, CG59987-02 DNA Sequence	CGCCGCTAGCATGACCAGCGCGTGTGCCCCGCGGCCCCAGCCGCTGGAGAAGGAG AACGACGGCTACTTTCGGAAGGCGTGTAAATCCCCCTGCACAAACCGGCGGAGTAAAT TGCAGAATCAAAGAGCTGCTTTGAATCAGCAGATCCTGAAAGCCGTGCGGATGAGGAC CGGAGCGGAAAACTTCTGAAAGTGGCCACAACTCAAAGGTGCGGGAGCAAGTGGCG CTGGAGCTGAGCTTCGTCAACTCAGACCTGCAGATGCTCAAGGAAGAGCTGGAGGGGC TGAACATCTCGGTGGGCGTCTATCAGAACACAGAGGAGGCATTACGATTCCCCTGAT TCCTCTTGGCCTGAAGGAAACGAAAGACGTGCACTTTGCAGTGCCTCTCAAGGATTTT ATCCTGGAACATTACAGTGAAGATGGCTATTTATATGAAGATGAAATTGCAGATCTTA TGGATCTGAGACAAGCTTGTGCGACGCTAGCCGGGATGAGGCCGGGTGGAAGTCTGT GATGACATACTTCATCCAGCTGGGCTTTGTGAGAGTGCATTCTTCCCGCCACACGG CAGATGGGACTCCTGTTCACTGGTATGACTCTCTACCGGGGTTCCGGTCAGCCAGC AGAACCCTGCTGCTGGAGAAGGCCAGTGTCTGTTCAACACTGGGGCCTCTACACCCA GATTGGGACCCGGTGGCATCGGCAGACGCAAGGCTGGGCTGGAGAGTGCCATAGATGCC TTTCAGAGAGCCGAGGGGTTTAAATTACCTGAAAGACACATTTACCCTACTCCAA GTTACGACATGAGCCCTGCCATGCTCAGCGTGTCTCGTCAAAATGATGCTTGCACAAGC CCAAGAAAGCGTGTGAGAAAATCAGCCTTCTGGGATCCGGAATGAATCTTTCATG CTGGTGAAGGTGGCTCAGGAGGCTGCTAAGGTGGGAGAGGTCTACCAACAGCTACACG CAGCCATGAGCCAGGCGCGGTGAAAGAGAATCCCCCTACTCTGGCCAGCTTAGC CTGGCTGAAGGCCACCACTACGCGGCCCTGGCCCACTACTTCACTGCCATCCTCCTC ATCGACCACCAGGTGAAGCCAGGCACGGATCTGGACCACCAGGAGAAGTGCTGTCCC AGCTCTACGACCACATGCCAGAGGGGCTGACACCCTTGGCCACACTGAAGAATGATCA GCAGCGCCGACAGCTGGGAAGTCCCACTTGCAGAGGCCATGGTCTCATACGAGGAG TCGGTGGCGGAGGCAAGCCTCTGCAAGAAGCTGCGGAGCATTGAGGTGCTACAGAAGG TGCTGTGTGCGGCACAGGAACGCTCCCGGCTCAGCTACGCCAGCACCAGGAGGAGGA TGACCTGTGAACCTGATCGACGCCCCAGTGTGTTGTCTAAACTGAGCAAGAGGTT GACATTATATTGCCCAAGTTCTCAAGCTGCAGCTACCGGACTTCTTCCAGAAGCTGG GCCCTTATCTGTGTTTTCGGCTAACAAAGCGGTGGACGCTCCTCGAAGCATCCGCTT CACTGCAGAAGAAGGGGACTTGGGGTTCACTTGAGAGGGAACGCCCCCTTCAGGTT CACTTCTGGATCCTTACTGCTCTGCTCGGTGGCAGGAGCCGGGAAGGAGATTATA TTGTCTCCATTAGCTTGTGGATTGTAAGTGGCTGACGCTGAGTGAGGTTATGAAGCT GCTGAAGAGCTTTGGCGAGGACGAGATCGAGATGAAAGTCTGTAGGCTCCTGGACTCC ACATCATCCATGCATAATAAGAGTGCCACATACTCCGTGGGAATGTAGAAAACGTA CCATGATCTGCTTAGCCATTGATGATGACGACAAAAGTATGATAAAACCAAGAAAATCTC CAAGAAGCTTTCCTTCCTGAGTTGGGGCACCACAAAGAACAGACAGAAAGTCAAGCCAGC ACCTTGTGCTTCCATCGGTGCGGGCTGCACGGCTCAGGTCAAGAAGAAGCTGCCCT CCCCCTTCAAGCTTCTCAACTCAGACAGTCTTGGTACTAATGTGAGGAAACAAACAT GTTCAAGGCCCGAACATTTC		
	ORF Start: ATG at 11	ORF Stop: TAG at 1844	
	SEQ ID NO: 352	611 aa	MW at 68613.9kD
NOV126b, CG59987-02 Protein Sequence	MTDALLPAAPQPLEKENDGYFRKGCNPLAQTRSKLQNRQALNQILKAVRMRTGAE NLLKVATNSKVRLELQMLKEEGLNISVGVYQNTTEEAFTIPLIPLG LKETKDVFVVLKDFILEHYSYEDGYLYEETADLMDLRQACRTPSRDEAGVELLMTY FIQLGFVESRFFPPTRQMGLLFTWYDSLTVGVPSQNLLEKASVLFNTGALYTIQIGT RCDRQTQAGLESAIDAFQRAAGVLNLYKDTFTHTPSYDMSPAMLSVLVKMMLAQAES VFEKISLPGIRNEFFMLVKVAQEAQVGEVYQQLHAAMSQAPVKENIPYSWASLACVK AHHYAALAHYFTAILLDHQQVPGTDLHQEKCLSQLYDHMPGLTPLATLKNDDQRR QLGKSHLRRAHHEESVREASLCKKLRSIEVLQKVLCAAQERSRLTYAQHQEEDLL NLIDAPSVAKTEQEVDIILPQFSKLTVTDFQKLGPLSVFSANKRWTPPRSIRFTA EGDLGFTLRGNAPVQVHFLDPYCSASVAGAREGDYIVSIQLVDCWKWLTLSFVMKLLKS FGEDEIEMKVVSLLDSTSSMHNKSATYSVGM		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 126B.

Table 126B. Comparison of NOV126a against NOV126b.		
Protein Sequence	NOV126a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV126b	1..611	585/612 (95%)
	1..611	590/612 (95%)

Further analysis of the NOV126a protein yielded the following properties shown in Table 126C.

Table 126C. Protein Sequence Properties NOV126a	
PSort analysis:	0.4500 probability located in cytoplasm; 0.3000 probability located in microbody (peroxisome); 0.1000 probability located in mitochondrial matrix space; 0.1000 probability located in lysosome (lumen)
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV126a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several homologous proteins shown in Table 126D.

Table 126D. Geneseq Results for NOV126a				
Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV126a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAU10192	Human prostate specific protein PSL22 - Homo sapiens, 686 aa. [WO200172962-A2, 04-OCT-2001]	1..686 1..686	660/687 (96%) 665/687 (96%)	0.0
AAB68561	Human GTP-binding associated protein #61 - Homo sapiens, 666 aa. [WO200105970-A2, 25-JAN-2001]	27..686 7..666	626/661 (94%) 633/661 (95%)	0.0
AAG64579	Human transcription termination factor binding protein 54 - Homo sapiens, 488 aa. [CN1297918-A, 06-	201..686 3..488	458/487 (94%) 464/487 (95%)	0.0
	tyrosine phosphatase, SH-PTD NO.2		252/253	

	[WO200063392-A1, 26-OCT-2000]			
AAU00869	Human cancer related protein 5 - Homo sapiens, 257 aa. [WO200118014-A1, 15-MAR-2001]	409..597 8..196	70/189 (37%) 102/189 (53%)	2e-27

In a BLAST search of public sequence databases, the NOV126a protein was found to have homology to the proteins shown in the BLASTP data in Table 126E.

Table 126E. Public BLASTP Results for NOV126a				
Protein Accession Number	Protein/Organism/Length	NOV126a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
Q96RU1	RHOPHILIN-LIKE PROTEIN - Homo sapiens (Human), 685 aa.	1..686 1..685	627/688 (91%) 640/688 (92%)	0.0
Q9DBN2	1300002E07RIK PROTEIN - Mus musculus (Mouse), 686 aa.	1..686 1..686	573/687 (83%) 616/687 (89%)	0.0
Q61085	GTP-RHO binding protein 1 (Rhopilin) - Mus musculus (Mouse), 643 aa.	16..596 20..580	273/583 (46%) 361/583 (61%)	e-135
Q9XYY9	RHOPHILIN - Drosophila melanogaster (Fruit fly), 718 aa.	21..615 31..674	248/654 (37%) 363/654 (54%)	e-110
Q96PV9	KIAA1929 PROTEIN - Homo sapiens (Human), 410 aa (fragment).	23..366 17..362	178/346 (51%) 241/346 (69%)	1e-93

PFam analysis predicts that the NOV126a protein contains the domains shown in the Table 126F.

Table 126F. Domain Analysis of NOV126a			
Pfam Domain	NOV126a Match Region	Identities/ Similarities for the Matched Region	Expect Value
HR1: domain 1 of 1	38..110	19/87 (22%) 53/87 (61%)	1.2e-05
BRO1: domain 1 of 1	111..263	60/172 (35%)	3.8e-56
PDZ: domain 1 of 1	136..595	9/84 (24%) 53/84 (63%)	0.0001

Example 127.

The NOV127 clone was analyzed, and the nucleotide and predicted polypeptide sequences are shown in Table 127A.

Table 127A. NOV127 Sequence Analysis

[illegible]

CG59971-01 Protein Sequence	<p>FVALPSHPADSPVILQLQFLFDVLQKTLSLKLHVHAGPGTGPICKIFFPKSLRHLELR GVPLHCLHGLRGIYSQLETLICSRSLQALEELLSSACGGDFCSALPWLALLSANFSYNA LTALDSSSLRLLSALRFLNLSHNQVQDCQGFMDLCELHHLDISYNRHLHVPRMGPGSA ALGVLLLRGNELRSLPGLEQLRNLRLHLDLAYNLLLEGHRELSPLWLLAELRLKLYLEGNP LWFHPEHRAATAQYLSPRARDAATGFLLDGKVLSTLDFQQTHTSLGLSPMGPPPLWPV GSTPETSGGPDLSDSLSSGGVVTQPLLHKVKSRRVRRASISEPSTDDPERTLNPSF AGWVQQHPELELMSSFRERFRNWLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGP DTAPRPSPPQEEARGPQESPKMSEEVRAEPQEEEEKEGKEEKEGEMVEQ3EEEAG EEEEEQDQKEVEAELCRPLLVCPLGEGVGRGECFLRVTS AHLFEVELQAARTLER LELQSLAAAEIEPEAQAGGPPLAAQGSDDLPGAPILSLRFSYICPDRLRRYLVLPEP AHAHVQELLAVLTPVTNVAREQLGEARDLLGRFQCLRCGHEFKPEEPRMGLDSEEGW RPLFQKTESPAVCNPGSDHVVLLAVSRGTNNRERKQGEQSLAPSASPVCHPPGHG DHLDRAKNSPPQAPSTRDHGSWSLSPAPERCLRSVDHRLRLFLDVEVFSDAQEEFQ CLKVPVALAGHTGEFMCLVVVSDRRLLYLLKVTGEMSEPPASWLQTLAVPLQDLSGIE LGLAGGSLRLLEWAAGAGRCVLLPRDARHCRAFLLELLGLVLSLPPAWNRNCVSATEEV TPQHRLLWPLEKSSLEARQFFYLRAFLVEGEASVQLMLPSTCLVSLLLTPSTLFLLD EDAAGSPAEPSPPAASGEASEKVPSPGPGPAVRVREQQPLSSLSVLLYRSPAPELRL LFYDEVSRLSEFWALRVVCQEQLTALLAWIREPWEEELFSLGLRTVIEALALDR</p>
	<p>SEQ ID NO: 355 3348 bp</p>
NOV127b, CG59971-02 DNA Sequence	<p>CGTCCCGTGGCCATGACGACCGCTCAGAGGAGCTCCCTGTGTGGAAGCTCGCGGGGT TGTGCGGGAGTCCCGGTATGTGGTCTGTCTGGCTGTAGCACCTGAGCCTGCTGAC TCCACACTGCAACAGCTGAACACGTATTTGAGCTGCACCTGGGGCCATGGGCCCT GGCCAGACAGGCTTTGTGGCTCTGCCCTCCCATCTGCCGACTCCCTGTATTCTTC AGCTTCAGTTCTCTTCATGTGCTGCAGAAAACACTTTCACTCAAGCTGGTCCATGT TGCTGGTCTGGCCCCACAGGGCCCATCAAGATTTTCCCTTCAAATCCCTTGGGCAC CTGGAGCTCCGAGGTGTTCCCTCCACTGTCTGCATGGCTCCGAGGCATCTACTCCC AGCTGGAGACCTGATTGTCAGCAGGAGCCTCCAGGCATTAGAGGAGCTCCTCTCAGC CTGCGGCGGCGACTTCTGCTCTGCCCTCCCTTGGCTGGCTCTGCTTTCTGCCAATTC AGCTACAATGCACTGACCGCCTTAGACAGCTCCCTGCGCCTCTGTGACGCTCTGCGTT TCTTGAACCTAAGCCACAATCAAGTCCAGGACTGTGAGGATTCCTGATGGATTGTG TGAGCTCCACCATCTGGACATCTCTATAATCGCCTGCATTGGTGCCAAGATGGGA CCCTCAGGGGCTGCTCTGGGGGTCTGATACTGCGAGGCAATGAGCTTCGGAGCCTGC CAGGCCTAGAGCAGCTGAGGAATCTGCGGCACCTGGATTGGCATACAACCTGTGGGA AGGACACCGGGAGCTGTCACTGTGGCTGCTGGCTGAGCTCCGCAAGCTCTACCTG GAGGGGAACCTCTTTGGTTCCACCTGAGCACCAGCAGCAGCTCACTTGTGAGCCTCT CACCCCGGGCCAGGGATGCTGCTACTGGCTTCTTCTCGATGGCAAGGTCTTGTCACT GACAGATTTTCAGCAGACTCACACATCTTGGGGCTCAGCCCCATGGGGCCACCTTTG CCCTGGCCAGTGGGGAGTACTCTGAAACCTCAGGTGGCCCTGACCTGAGTGACAGCC TCTCTCAGGGGGTGTGTGACCCAGCCCCGCTTTCATAAGGTTAAGAGCCGAGTCCG TGTGAGGCGGGCAAGCATCTCTGAACCCAGTGATACGGACCCGGAGCCCCGAACCTG AACCCCTCTCCGGCTGTTGGTTGCTGTCAGCAGCACCAGGAGCTGGAGCTCATGAGCA GCTTCCGGGAACGTTTCGGCCGCAACTGGCTGCACTACAGGAGTCACTTGTGAGCCTC CGGAACCCCTCTGCGGGCCACCCCACTACTTCTGCAACCCAGTGCACCTCCAGCCAGC TCCAGGGGCCCCGACATGCACCCAGACCTTCACCCCGCAGGAGGAGCCAGAGGGCC CCCAGGAGTCACACAGAAAATGTGAGAGGAGTCAAGGCGGAGCCACAGGAGGAGGA AGAGGAGAAGGAGGGAAGGAGGAGAAGGAGGAGGAGGAGAGTGTGAACAGGGAGAA GAGGAGGCAGGAGGAGGAGAAGAGGAGCAGGACCAGAAGGAAGTGAAGCGGAAC TCTGTGCGCCCTTGTGGTGTGTCCCTGGAGGGGCTGAGGGCGTACGGGGCAGGGA ATGCTTTCTCAGGGTCACTTCTGCCACCTGTTTGAAGTGGAACCTCAAGCAGCTCGC ACCTTGGAGCGACTGGAGCTCCAGAGTCTGGAGGCAGCTGAGATAGAGCCGAGGCCCC AGGCCAGAGGTGCCCCAGGCCACGGGCTCAGATCTGCTCCCTGGAGCCCCATCTCT CAGTCTGCGCTTCTCTACATCTGCCCTGACCGGAGTTGCGTCTGCTATTGTGTGCTG GAGCCTGATGCCACGCAGCTGTCCAGGAGCTGCTGCGGTGTGACCCGAGTCAACCA ATGTGGCTCGGGAACAGCTTGGGAGGCCAGGACCTCTGTGGGTAGATTTCAGTG TCTACGCTGTGGCCATGAGTTCAAGCCAGAGGAGCCAGGATGGGATTAGACAGTGAG GAAGGCTGGAGGCTCTGTTTCAAAAGACAGAATCTCTGCTGTGTCTTAACTGTG GTAGTGACCAAGTGGTTCTCTCTGCTGTGTCTCGGGGAACCCCAACAGGAGCGGAA ACAGGGAGAGCAGTCTCTGGCTCTTCTCCGTCTGCCAGCCCTGTCTGCCACCCCTCT GGCCATGGTGACCACTTGACAGGGCCAAGAACAGCCACCTCAGGCACCGAGCACC GTGACCATGGTAGTTGGAGCCTCAGTCCCGCCCTGAGCGCTGTGGCTCCGCTCTGT GGACCACTGACTCCGGCTCTTCTGGATGTTGAGGTGTTACGCGATGCCAGGAGGAG TTCCAGTGTGCTCAAGGTCCAGTGGCATTGGCAGGCCACACTGGGAGTTCATGT GCCTTGTGGTTGTGTCTGACCGCAGGCTGTACCTGTTGAAGGTGACTGGGAGATGAG TGAGCCTCCAGCTAGCTGGCTGCAGCTGACCTGGCTGTTCCCTGCAGGATCTGAGT GGCATAGAGCTGGGCTGGCAGGCCAGAGCCTGCGCTAGAGTGGGAGCTGGGCGG GCGCGTGTGTGCTGCTGCCCTGAGATGCCAGGCATTGCCGGCCCTTCTAGAGGAGCT TTTGGTGTCTTGCAGTCTCTGCCCTGCTGGAGGAACCTGTTGAGTGCACAGAG GAGGAGGTCAACCCCGCAGCCGGCTCTGGCCATTGCTGGAAAAGACTCATCTTGG</p>

	GCTGTTTTCCATCGGACTCCGGACAGTGATCCAAGAGGCGCTGGCCCTTGACCGATGA GGGTCCCACGCTGACCTTGGCCCTGACCTCAGGAGCCACGCT		
	ORF Start: ATG at 13	ORF Stop: TGA at 3304	
	SEQ ID NO: 356	1097 aa	MW at 121064.1kD
NOV127b, CG59971-02 Protein Sequence	MTTAQRDSSLWKLGLLRESGDVVLSCGSTLSLLTPTLQQLNHVFELHLGPWPGQTG FVALPSHFADSPVILQLQFLFDVLQKTLCLKLVHVAGPGPTGPIKIFPFKSLRHELR GVPLHCLHGLRGIYSQLETICSRSLQALEELLSACGGDFCSALPWLALLSANFSYNA LTALDSSLRLLSALRFLNLSHNQVQDCQGFLMDLCELHHLDISYNRLHLVPRMGPSGA ALGVILLRGNELRSLPCLEQLRNLRLHLDIAYNLEGHRELSPLWLLAEFLKLYLEGNP LWFHPHRAATAQYLSPRARDAATGFLLDGKVLSTDFQQTHTSLGLSPMGPPLPWFV GSTPETSPPDLSDSLSSGGVVTQPLLHKVKSRVVRASISEPSDTPPEPRTLNPS AGWVQVQHPLELMSSFRERFGRNLQYRSHLEPSGNPLPATPTTSAPSAPPASSQGP DTAPRPSPPQEEARGPQESPOKMSEEVRAEPQEEEEKEGKEEKEGEMVEQGEAEAG EEEEEQDQKEVEAELCRPLLVCPLGPEGVGRGECFLRVTSAHLEFEVLQAARTLER LELQSLAEAEIEPEAQQRSPRPTGSDLLPGAPILSLRFSYICPDQLRRYLVLEPDA HAAVQELLAVLTPVTNVAREQLGEARDLLGRFQCLRCGHEFKPEEPRMGLDSEEGWR PLFQKTESPAVCPNCGSDHVVLLAVSRGTPNRERKQGEQSLAPSPASPVCHPPGHGD HLDRAKNSPPQAPSTRDHGSWSLSPAPERCGLSVDHRLRLFLDVEVFSDAQEEFQCC LKVPVALAGHTGEFMCVLVVSDDRLLYLLKVTGEMSEPPASWLQTLAVPLQDLSGIEL GLAGQSLRLAWAAGAGRCVLLPRDARHCRAFLEELLGVLSLPPAARNVCVSATEEVET PQHRLWPLEKDSSLEARQFFYLRAFLVEGEASVQLMLPSTCLVSLLLTPSTLFLLE DAAGSPAEPSPPAASGEASEKVPSPGPGFAVRVREQQPLSSLSVLLYRSAPEDLRL FYDEVSRLESFALRVVCQEQLTALLAWIREPWEELFSIGLRTVIEQALALDR		

Sequence comparison of the above protein sequences yields the following sequence relationships shown in Table 127B.

Table 127B. Comparison of NOV127a against NOV127b.		
Protein Sequence	NOV127a Residues/ Match Residues	Identities/ Similarities for the Matched Region
NOV127b	1..1098	891/1098 (81%)
	1..1097	891/1098 (81%)

Further analysis of the NOV127a protein yielded the following properties shown in Table 127C.

Table 127C. Protein Sequence Properties NOV127a	
PSort analysis:	0.5163 probability located in mitochondrial matrix space; 0.3000 probability located in microbody (peroxisome); 0.2442 probability located in mitochondrial inner membrane; 0.2442 probability located in mitochondrial intermembrane space
SignalP analysis:	No Known Signal Sequence Predicted

A search of the NOV127a protein against the Geneseq database, a proprietary database that contains sequences published in patents and patent publication, yielded several

Table 127D. Geneseq Results for NOV127a

Geneseq Identifier	Protein/Organism/Length [Patent #, Date]	NOV127a Residues/ Match Residues	Identities/ Similarities for the Matched Region	Expect Value
AAM39827	Human polypeptide SEQ ID NO 2972 - Homo sapiens, 169 aa. [WO200153312-A1, 26-JUL-2001]	375..528 14..167	140/154 (90%) 145/154 (93%)	3e-78
AAM41613	Human polypeptide SEQ ID NO 6544 - Homo sapiens, 184 aa. [WO200153312-A1, 26-JUL-2001]	375..528 29..182	140/154 (90%) 145/154 (93%)	4e-78
AAU19764	Human novel extracellular matrix protein, Seq ID No 414 - Homo sapiens, 211 aa. [WO200155368-A1, 02-AUG-2001]	444..647 13..209	157/207 (75%) 160/207 (76%)	2e-75
ABB19833	Protein #1832 encoded by probe for measuring heart cell gene expression - Homo sapiens, 127 aa. [WO200157274-A2, 09-AUG-2001]	409..535 1..127	127/127 (100%) 127/127 (100%)	2e-70
AAM67606	Human bone marrow expressed probe encoded protein SEQ ID NO: 27912 - Homo sapiens, 127 aa. [WO200157276-A2, 09-AUG-2001]	409..535 1..127	127/127 (100%) 127/127 (100%)	2e-70

In a BLAST search of public sequence databases, the NOV127a protein was found to have homology to the proteins shown in the BLASTP data in Table 127E.

Table 127E. Public BLASTP Results for NOV127a				
Protein Accession Number	Protein/Organism/Length	NOV127a Residues/ Match Residues	Identities/ Similarities for the Matched Portion	Expect Value
AAL49726	LKBI-INTERACTING PROTEIN 1 - Homo sapiens (Human), 1099 aa.	1..1098 12..1099	1077/1098 (98%) 1078/1098 (98%)	0.0
Q96PY9	KIAA1898 PROTEIN - Homo sapiens (Human), 1013 aa (fragment).	76..1098 1..1013	1003/1023 (98%) 1003/1023 (98%)	0.0
Q96CN3	SIMILAR TO RIKEN CDNA	288..1098	793/811 (97%)	0.0
Q9DBT7				0.0

	musculus (Mouse), 1072 aa.	1..1072	895/1098 (81%)	
Q9VMK9	CG9044 PROTEIN - Drosophila melanogaster (Fruit fly), 1289 aa.	12..433 8..463	139/459 (30%) 220/459 (47%)	6e-38

PFam analysis predicts that the NOV127a protein contains the domains shown in the Table 127F.

Table 127F. Domain Analysis of NOV127a			
Pfam Domain	NOV127a Match Region	Identities/ Similarities for the Matched Region	Expect Value
LRR: domain 1 of 5	164..186	7/25 (28%) 15/25 (60%)	2.5e+02
LRR: domain 2 of 5	187..209	6/25 (24%) 16/25 (64%)	2.5e+02
LRR: domain 3 of 5	210..231	8/25 (32%) 13/25 (52%)	83
LRR: domain 4 of 5	233..254	9/25 (36%) 17/25 (68%)	16
LRR: domain 5 of 5	255..279	10/27 (37%) 19/27 (70%)	22
Pkinase_C: domain 1 of 1	620..629	5/11 (45%) 9/11 (82%)	8.9
rubredoxin: domain 1 of 2	669..686	5/18 (28%) 13/18 (72%)	4.6
rubredoxin: domain 2 of 2	708..713	5/6 (83%) 6/6 (100%)	1.2e+03

Example B: Sequencing Methodology and Identification of NOVX Clones

1. **GeneCalling™ Technology:** This is a proprietary method of performing differential

database query (Nature Biotechnology 17: 198-202 (1999)). cDNA was derived from various

human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then digested with up to as many as 120 pairs of restriction enzymes and pairs of linker-adaptors specific for each pair of restriction enzymes were ligated to the appropriate end. The restriction digestion generates a mixture of unique cDNA gene fragments. Limited PCR amplification is performed with primers homologous to the linker adapter sequence where one primer is biotinylated and the other is fluorescently labeled. The doubly labeled material is isolated and the fluorescently labeled single strand is resolved by capillary gel electrophoresis. A computer algorithm compares the electropherograms from an experimental and control group for each of the restriction digestions. This and additional sequence-derived information is used to predict the identity of each differentially expressed gene fragment using a variety of genetic databases. The identity of the gene fragment is confirmed by additional, gene-specific competitive PCR or by isolation and sequencing of the gene fragment.

2. SeqCalling™ Technology: cDNA was derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then sequenced using CuraGen's proprietary SeqCalling technology. Sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions, deletions and other sequence variations.

The NOVX nucleic acid sequences are derived by laboratory screening of cDNA library by the two-hybrid approach. cDNA fragments covering either the full length of the DNA sequence, or part of the sequence, or both, are sequenced. In silico prediction was based on sequences available in CuraGen Corporation's proprietary sequence databases or in the public human sequence databases, and provided either the full length DNA sequence, or some portion thereof.

The laboratory screening was performed using the methods summarized below:

cDNA libraries were derived from various human samples representing multiple tissue types, normal and diseased states, physiological states, and developmental states from different donors. Samples were obtained as whole tissue, primary cells or tissue cultured primary cells or cell lines. Cells and cell lines may have been treated with biological or chemical agents that regulate gene expression, for example, growth factors, chemokines or steroids. The cDNA thus derived was then directionally cloned into the appropriate two-hybrid vector (Gal4-activation domain (Gal4-AD) fusion). Such cDNA libraries as well as commercially available cDNA libraries from Clontech (Palo Alto, CA) were then transferred from E.coli into a CuraGen Corporation proprietary yeast strain (disclosed in U. S. Patents 6,057,101 and 6,083,693, incorporated herein by reference in their entireties).

Gal4-binding domain (Gal4-BD) fusions of a CuraGen Corporation proprietary library of human sequences was used to screen multiple Gal4-AD fusion cDNA libraries resulting in the selection of yeast hybrid diploids in each of which the Gal4-AD fusion contains an individual cDNA. Each sample was amplified using the polymerase chain reaction (PCR) using non-specific primers at the cDNA insert boundaries. Such PCR product was sequenced; sequence traces were evaluated manually and edited for corrections if appropriate. cDNA sequences from all samples were assembled together, sometimes including public human sequences, using bioinformatic programs to produce a consensus sequence for each assembly. Each assembly is included in CuraGen Corporation's database. Sequences were included as components for assembly when the extent of identity with another component was at least 95% over 50 bp. Each assembly represents a gene or portion thereof and includes information on variants, such as splice forms single nucleotide polymorphisms (SNPs), insertions.

Physical clone: the cDNA fragment derived by the screening procedure, covering the entire open reading frame is, as a recombinant DNA, cloned into pACT2 plasmid (Clontech) used to make the cDNA library. The recombinant plasmid is inserted into the host and selected by the yeast hybrid diploid generated during the screening procedure by the mating of both CuraGen Corporation proprietary yeast strains N106' and YULH (U. S. Patents 6,057,101 and 6,083,693).

4. RACE: Techniques based on the polymerase chain reaction such as rapid amplification of cDNA ends (RACE), were used to isolate or complete the predicted sequence of the cDNA of the invention. Usually multiple clones were sequenced from one or more human samples to derive the sequences for fragments. Various human tissue samples from different donors were used for the RACE reaction. The sequences derived from these procedures were included in the SeqCalling Assembly process described in preceding paragraphs.

5. Exon Linking: The NOVX target sequences identified in the present invention were subjected to the exon linking process to confirm the sequence. PCR primers were designed by starting at the most upstream sequence available, for the forward primer, and at the most downstream sequence available for the reverse primer. **Table B1** shows the sequences of the PCR primers used for obtaining different clones. In each case, the sequence was examined, walking inward from the respective termini toward the coding sequence, until a suitable sequence that is either unique or highly selective was encountered, or, in the case of the reverse primer, until the stop codon was reached. Such primers were designed based on in silico predictions for the full length cDNA, part (one or more exons) of the DNA or protein sequence of the target sequence, or by translated homology of the predicted exons to closely related human sequences from other species. These primers were then employed in PCR amplification based on the following pool of human cDNAs: adrenal gland, bone marrow, brain - amygdala, brain - cerebellum, brain - hippocampus, brain - substantia nigra, brain - thalamus, brain -whole, fetal brain, fetal kidney, fetal liver, fetal lung, heart, kidney, lymphoma - Raji, mammary gland, pancreas, pituitary gland, placenta, prostate, salivary gland, skeletal muscle, small intestine, spinal cord, spleen, stomach, testis, thvroid, trachea.

from Invitrogen. The resulting bacterial clone has an insert covering the entire open reading

frame cloned into the pCR2.1 vector. The resulting sequences from all clones were assembled with themselves, with other fragments in CuraGen Corporation's database and with public ESTs. Fragments and ESTs were included as components for an assembly when the extent of their identity with another component of the assembly was at least 95% over 50 bp. In addition, sequence traces were evaluated manually and edited for corrections if appropriate. These procedures provide the sequence reported herein.

6. Physical Clone:

Exons were predicted by homology and the intron/exon boundaries were determined using standard genetic rules. Exons were further selected and refined by means of similarity determination using multiple BLAST (for example, tBlastN, BlastX, and BlastN) searches, and, in some instances, GeneScan and Grail. Expressed sequences from both public and proprietary databases were also added when available to further define and complete the gene sequence. The DNA sequence was then manually corrected for apparent inconsistencies thereby obtaining the sequences encoding the full-length protein.

The PCR product derived by exon linking, covering the entire open reading frame, was cloned into the pCR2.1 vector from Invitrogen to provide clones used for expression and screening purposes.

Example C: Quantitative expression analysis of clones in various cells and tissues

The quantitative expression of various clones was assessed using microtiter plates containing RNA samples from a variety of normal and pathology-derived cells, cell lines and tissues using real time quantitative PCR (RTQ PCR). RTQ PCR was performed on an Applied Biosystems ABI PRISM® 7700 or an ABI PRISM® 7900 HT Sequence Detection System. Various collections of samples are assembled on the plates, and referred to as Panel 1 (containing normal tissues and cancer cell lines), Panel 2 (containing samples derived from tissues from normal and cancer sources), Panel 3 (containing cancer cell lines), Panel 4 (containing cells and cell lines from normal tissues and cells related to inflammatory conditions), Panel 5D/5I (containing human tissues and cell lines with an emphasis on

cell lines derived from Alzheimer's disease, Parkinson's disease, Huntington's disease, and amyotrophic lateral sclerosis).

Panel 5D/5I (containing human tissues and cell lines with an emphasis on normal and diseased brains) and CNS neurodegeneration panel (containing samples from normal and Alzheimer's diseased brains).

RNA integrity from all samples is controlled for quality by visual assessment of agarose gel electropherograms using 28S and 18S ribosomal RNA staining intensity ratio as a guide (2:1 to 2.5:1 28s:18s) and the absence of low molecular weight RNAs that would be indicative of degradation products. Samples are controlled against genomic DNA contamination by RTQ PCR reactions run in the absence of reverse transcriptase using probe and primer sets designed to amplify across the span of a single exon.

First, the RNA samples were normalized to reference nucleic acids such as constitutively expressed genes (for example, β -actin and GAPDH). Normalized RNA (5 μ l) was converted to cDNA and analyzed by RTQ-PCR using One Step RT-PCR Master Mix Reagents (Applied Biosystems; Catalog No. 4309169) and gene-specific primers according to the manufacturer's instructions.

In other cases, non-normalized RNA samples were converted to single strand cDNA (sscDNA) using Superscript II (Invitrogen Corporation; Catalog No. 18064-147) and random hexamers according to the manufacturer's instructions. Reactions containing up to 10 μ g of total RNA were performed in a volume of 20 μ l and incubated for 60 minutes at 42°C. This reaction can be scaled up to 50 μ g of total RNA in a final volume of 100 μ l. sscDNA samples are then normalized to reference nucleic acids as described previously, using 1X TaqMan® Universal Master mix (Applied Biosystems; catalog No. 4324020), following the manufacturer's instructions.

Probes and primers were designed for each assay according to Applied Biosystems Primer Express Software package (version I for Apple Computer's Macintosh Power PC) or a similar algorithm using the target sequence as input. Default settings were used for reaction conditions and the following parameters were set before selecting primers: primer concentration = 250 nM, primer melting temperature (T_m) range = 58°-60°C, primer optimal T_m = 59°C, maximum primer difference = 2°C, probe does not have 5'G, probe T_m must be 10°C greater than primer T_m , amplicon size 75bp to 100bp. The probes and primers selected (see below) were synthesized by Synthegen (Houston, TX, USA). Probes were double purified by HPLC to remove uncoupled dye and evaluated by mass spectroscopy to verify coupling of reporter and quencher dyes to the 5' and 3' ends of the probe respectively. Their final

PCR conditions: When working with RNA samples, normalized RNA from each tissue and each cell line was spotted in each well of either a 96 well or a 384-well PCR plate (Applied Biosystems). PCR cocktails included either a single gene specific probe and primers set, or two multiplexed probe and primers sets (a set specific for the target clone and another gene-specific set multiplexed with the target probe). PCR reactions were set up using TaqMan® One-Step RT-PCR Master Mix (Applied Biosystems, Catalog No. 4313803) following manufacturer's instructions. Reverse transcription was performed at 48°C for 30 minutes followed by amplification/PCR cycles as follows: 95°C 10 min, then 40 cycles of 95°C for 15 seconds, 60°C for 1 minute. Results were recorded as CT values (cycle at which a given sample crosses a threshold level of fluorescence) using a log scale, with the difference in RNA concentration between a given sample and the sample with the lowest CT value being represented as 2 to the power of delta CT. The percent relative expression is then obtained by taking the reciprocal of this RNA difference and multiplying by 100.

When working with sscDNA samples, normalized sscDNA was used as described previously for RNA samples. PCR reactions containing one or two sets of probe and primers were set up as described previously, using 1X TaqMan® Universal Master mix (Applied Biosystems; catalog No. 4324020), following the manufacturer's instructions. PCR amplification was performed as follows: 95°C 10 min, then 40 cycles of 95°C for 15 seconds, 60°C for 1 minute. Results were analyzed and processed as described previously.

Panels 1, 1.1, 1.2, and 1.3D

The plates for Panels 1, 1.1, 1.2 and 1.3D include 2 control wells (genomic DNA control and chemistry control) and 94 wells containing cDNA from various samples. The samples in these panels are broken into 2 classes: samples derived from cultured cell lines and samples derived from primary normal tissues. The cell lines are derived from cancers of the following types: lung cancer, breast cancer, melanoma, colon cancer, prostate cancer, CNS cancer, squamous cell carcinoma, ovarian cancer, liver cancer, renal cancer, gastric cancer and pancreatic cancer. Cell lines used in these panels are widely available through the American

comprised of samples derived from all major organ systems from single adult individuals or

fetuses. These samples are derived from the following organs: adult skeletal muscle, fetal skeletal muscle, adult heart, fetal heart, adult kidney, fetal kidney, adult liver, fetal liver, adult lung, fetal lung, various regions of the brain, the spleen, bone marrow, lymph node, pancreas, salivary gland, pituitary gland, adrenal gland, spinal cord, thymus, stomach, small intestine, colon, bladder, trachea, breast, ovary, uterus, placenta, prostate, testis and adipose.

In the results for Panels 1, 1.1, 1.2 and 1.3D, the following abbreviations are used:

ca. = carcinoma,
* = established from metastasis,
met = metastasis,
s cell var = small cell variant,
non-s = non-sm = non-small,
squamous = squamous,
pl. eff = pl effusion = pleural effusion,
glio = glioma,
astro = astrocytoma, and
neuro = neuroblastoma.

General_screening_panel_v1.4

The plates for Panel 1.4 include 2 control wells (genomic DNA control and chemistry control) and 94 wells containing cDNA from various samples. The samples in Panel 1.4 are broken into 2 classes: samples derived from cultured cell lines and samples derived from primary normal tissues. The cell lines are derived from cancers of the following types: lung cancer, breast cancer, melanoma, colon cancer, prostate cancer, CNS cancer, squamous cell carcinoma, ovarian cancer, liver cancer, renal cancer, gastric cancer and pancreatic cancer. Cell lines used in Panel 1.4 are widely available through the American Type Culture Collection (ATCC), a repository for cultured cell lines, and were cultured using the conditions recommended by the ATCC. The normal tissues found on Panel 1.4 are comprised of pools of samples derived from all major organ systems from 2 to 5 different adult individuals or fetuses. These samples are derived from the following organs: adult skeletal muscle, fetal skeletal muscle, adult heart, fetal heart, adult kidney, fetal kidney, adult liver, fetal liver, adult lung, fetal lung, various regions of the brain, the spleen, bone marrow, lymph node, pancreas, salivary gland, pituitary gland, adrenal gland, spinal cord, thymus, stomach, small intestine,

Panels 2D and 2.2

The plates for Panels 2D and 2.2 generally include 2 control wells and 94 test samples composed of RNA or cDNA isolated from human tissue procured by surgeons working in close cooperation with the National Cancer Institute's Cooperative Human Tissue Network (CHTN) or the National Disease Research Initiative (NDRI). The tissues are derived from human malignancies and in cases where indicated many malignant tissues have "matched margins" obtained from noncancerous tissue just adjacent to the tumor. These are termed normal adjacent tissues and are denoted "NAT" in the results below. The tumor tissue and the "matched margins" are evaluated by two independent pathologists (the surgical pathologists and again by a pathologist at NDRI or CHTN). This analysis provides a gross histopathological assessment of tumor differentiation grade. Moreover, most samples include the original surgical pathology report that provides information regarding the clinical stage of the patient. These matched margins are taken from the tissue surrounding (i.e. immediately proximal) to the zone of surgery (designated "NAT", for normal adjacent tissue, in Table RR). In addition, RNA and cDNA samples were obtained from various human tissues derived from autopsies performed on elderly people or sudden death victims (accidents, etc.). These tissues were ascertained to be free of disease and were purchased from various commercial sources such as Clontech (Palo Alto, CA), Research Genetics, and Invitrogen.

Panel 3D

The plates of Panel 3D are comprised of 94 cDNA samples and two control samples. Specifically, 92 of these samples are derived from cultured human cancer cell lines, 2 samples of human primary cerebellar tissue and 2 controls. The human cell lines are generally obtained from ATCC (American Type Culture Collection), NCI or the German tumor cell bank and fall into the following tissue groups: Squamous cell carcinoma of the tongue, breast cancer, prostate cancer, melanoma, epidermoid carcinoma, sarcomas, bladder carcinomas, pancreatic cancers, kidney cancers, leukemias/lymphomas, ovarian/uterine/cervical, gastric, colon, lung and CNS cancer cell lines. In addition, there are two independent samples of cerebellum. These cells are all cultured under standard recommended conditions and RNA extracted using the standard procedures. The cell lines in panel 3D and 1-3D are of the most common cell lines

Panels 4D, 4R, and 4.1D

Panel 4 includes samples on a 96 well plate (2 control wells, 94 test samples) composed of RNA (Panel 4R) or cDNA (Panels 4D/4.1D) isolated from various human cell lines or tissues related to inflammatory conditions. Total RNA from control normal tissues such as colon and lung (Stratagene, La Jolla, CA) and thymus and kidney (Clontech) was employed. Total RNA from liver tissue from cirrhosis patients and kidney from lupus patients was obtained from BioChain (Biochain Institute, Inc., Hayward, CA). Intestinal tissue for RNA preparation from patients diagnosed as having Crohn's disease and ulcerative colitis was obtained from the National Disease Research Interchange (NDRI) (Philadelphia, PA).

Astrocytes, lung fibroblasts, dermal fibroblasts, coronary artery smooth muscle cells, small airway epithelium, bronchial epithelium, microvascular dermal endothelial cells, microvascular lung endothelial cells, human pulmonary aortic endothelial cells, human umbilical vein endothelial cells were all purchased from Clonetics (Walkersville, MD) and grown in the media supplied for these cell types by Clonetics. These primary cell types were activated with various cytokines or combinations of cytokines for 6 and/or 12-14 hours, as indicated. The following cytokines were used; IL-1 beta at approximately 1-5ng/ml, TNF alpha at approximately 5-10ng/ml, IFN gamma at approximately 20-50ng/ml, IL-4 at approximately 5-10ng/ml, IL-9 at approximately 5-10ng/ml, IL-13 at approximately 5-10ng/ml. Endothelial cells were sometimes starved for various times by culture in the basal media from Clonetics with 0.1% serum.

Mononuclear cells were prepared from blood of employees at CuraGen Corporation, using Ficoll. LAK cells were prepared from these cells by culture in DMEM 5% FCS (Hyclone), 100µM non essential amino acids (Gibco/Life Technologies, Rockville, MD), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco) and Interleukin 2 for 4-6 days. Cells were then either activated with 10-20ng/ml PMA and 1-2µg/ml ionomycin, IL-12 at 5-10ng/ml, IFN gamma at 20-50ng/ml and IL-18 at 5-10ng/ml for 6 hours. In some cases, mononuclear cells were cultured for 4-5 days in DMEM 5% FCS (Hyclone), 100µM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5×10^{-5} M (Gibco), and 10mM Hepes (Gibco) with PHA (phytohemagglutinin) or PWM (pokeweed mitogen) at approximately 5µg/ml. Samples were

and mixing the isolated mononuclear cells to a final concentration of approximately 2×10^6 cells/ml in DMEM 5% FCS (Hyclone), 100µM non essential amino acids (Gibco), 1mM

sodium pyruvate (Gibco), mercaptoethanol ($5.5 \times 10^{-5} \text{M}$) (Gibco), and 10mM Hepes (Gibco). The MLR was cultured and samples taken at various time points ranging from 1- 7 days for RNA preparation.

Monocytes were isolated from mononuclear cells using CD14 Miltenyi Beads, +ve VS selection columns and a Vario Magnet according to the manufacturer's instructions. Monocytes were differentiated into dendritic cells by culture in DMEM 5% fetal calf serum (FCS) (Hyclone, Logan, UT), 100 μM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol $5.5 \times 10^{-5} \text{M}$ (Gibco), and 10mM Hepes (Gibco), 50ng/ml GM-CSF and 5ng/ml IL-4 for 5-7 days. Macrophages were prepared by culture of monocytes for 5-7 days in DMEM 5% FCS (Hyclone), 100 μM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol $5.5 \times 10^{-5} \text{M}$ (Gibco), 10mM Hepes (Gibco) and 10% AB Human Serum or MCSF at approximately 50ng/ml. Monocytes, macrophages and dendritic cells were stimulated for 6 and 12-14 hours with lipopolysaccharide (LPS) at 100ng/ml. Dendritic cells were also stimulated with anti-CD40 monoclonal antibody (Pharmingen) at 10 $\mu\text{g/ml}$ for 6 and 12-14 hours.

CD4 lymphocytes, CD8 lymphocytes and NK cells were also isolated from mononuclear cells using CD4, CD8 and CD56 Miltenyi beads, positive VS selection columns and a Vario Magnet according to the manufacturer's instructions. CD45RA and CD45RO CD4 lymphocytes were isolated by depleting mononuclear cells of CD8, CD56, CD14 and CD19 cells using CD8, CD56, CD14 and CD19 Miltenyi beads and positive selection. CD45RO beads were then used to isolate the CD45RO CD4 lymphocytes with the remaining cells being CD45RA CD4 lymphocytes. CD45RA CD4, CD45RO CD4 and CD8 lymphocytes were placed in DMEM 5% FCS (Hyclone), 100 μM non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol $5.5 \times 10^{-5} \text{M}$ (Gibco), and 10mM Hepes (Gibco) and plated at 10^6 cells/ml onto Falcon 6 well tissue culture plates that had been coated overnight with 0.5 $\mu\text{g/ml}$ anti-CD28 (Pharmingen) and 3 $\mu\text{g/ml}$ anti-CD3 (OKT3, ATCC) in PBS. After 6 and 24 hours, the cells were harvested for RNA preparation. To prepare chronically activated CD8 lymphocytes, we activated the isolated CD8 lymphocytes for 4 days on anti-CD28 and anti-CD3 coated plates and then harvested the cells and expanded them in DMEM 5% FCS

cells were then activated again with plate binding anti-CD3 and anti-CD28 for 4 days and expanded as before. RNA was isolated 6 and 24 hours after the second activation and after 4

days of the second expansion culture. The isolated NK cells were cultured in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5x10⁻⁵M (Gibco), and 10mM Hepes (Gibco) and IL-2 for 4-6 days before RNA was prepared.

To obtain B cells, tonsils were procured from NDRI. The tonsil was cut up with sterile dissecting scissors and then passed through a sieve. Tonsil cells were then spun down and resuspended at 10⁶cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5x10⁻⁵M (Gibco), and 10mM Hepes (Gibco). To activate the cells, we used PWM at 5 μ g/ml or anti-CD40 (Pharmingen) at approximately 10 μ g/ml and IL-4 at 5-10ng/ml. Cells were harvested for RNA preparation at 24,48 and 72 hours.

To prepare the primary and secondary Th1/Th2 and Tr1 cells, six-well Falcon plates were coated overnight with 10 μ g/ml anti-CD28 (Pharmingen) and 2 μ g/ml OKT3 (ATCC), and then washed twice with PBS. Umbilical cord blood CD4 lymphocytes (Poietic Systems, German Town, MD) were cultured at 10⁵-10⁶cells/ml in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5x10⁻⁵M (Gibco), 10mM Hepes (Gibco) and IL-2 (4ng/ml). IL-12 (5ng/ml) and anti-IL4 (1 μ g/ml) were used to direct to Th1, while IL-4 (5ng/ml) and anti-IFN gamma (1 μ g/ml) were used to direct to Th2 and IL-10 at 5ng/ml was used to direct to Tr1. After 4-5 days, the activated Th1, Th2 and Tr1 lymphocytes were washed once in DMEM and expanded for 4-7 days in DMEM 5% FCS (Hyclone), 100 μ M non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol 5.5x10⁻⁵M (Gibco), 10mM Hepes (Gibco) and IL-2 (1ng/ml). Following this, the activated Th1, Th2 and Tr1 lymphocytes were re-stimulated for 5 days with anti-CD28/OKT3 and cytokines as described above, but with the addition of anti-CD95L (1 μ g/ml) to prevent apoptosis. After 4-5 days, the Th1, Th2 and Tr1 lymphocytes were washed and then expanded again with IL-2 for 4-7 days. Activated Th1 and Th2 lymphocytes were maintained in this way for a maximum of three cycles. RNA was prepared from primary and secondary Th1, Th2 and Tr1 after 6 and 24 hours following the second and third activations with plate bound anti-CD3 and anti-CD28 mAbs and 4 days into the second and

third activation cycles.

Following cytokine treatment, cells were seeded into 96 well plates (Corning Costar).

KU-812. EOL cells were further differentiated by culture in 0.1mM dbcAMP at 5x10⁵ cells/ml

for 8 days, changing the media every 3 days and adjusting the cell concentration to 5×10^5 cells/ml. For the culture of these cells, we used DMEM or RPMI (as recommended by the ATCC), with the addition of 5% FCS (Hyclone), $100 \mu\text{M}$ non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol $5.5 \times 10^{-5} \text{M}$ (Gibco), 10mM Hepes (Gibco). RNA was either prepared from resting cells or cells activated with PMA at 10ng/ml and ionomycin at $1 \mu\text{g/ml}$ for 6 and 14 hours. Keratinocyte line CCD106 and an airway epithelial tumor line NCI-H292 were also obtained from the ATCC. Both were cultured in DMEM 5% FCS (Hyclone), $100 \mu\text{M}$ non essential amino acids (Gibco), 1mM sodium pyruvate (Gibco), mercaptoethanol $5.5 \times 10^{-5} \text{M}$ (Gibco), and 10mM Hepes (Gibco). CCD106 cells were activated for 6 and 14 hours with approximately 5 ng/ml TNF alpha and 1 ng/ml IL-1 beta, while NCI-H292 cells were activated for 6 and 14 hours with the following cytokines: 5 ng/ml IL-4, 5 ng/ml IL-9, 5 ng/ml IL-13 and 25 ng/ml IFN gamma.

For these cell lines and blood cells, RNA was prepared by lysing approximately 10^7 cells/ml using Trizol (Gibco BRL). Briefly, 1/10 volume of bromochloropropane (Molecular Research Corporation) was added to the RNA sample, vortexed and after 10 minutes at room temperature, the tubes were spun at $14,000 \text{ rpm}$ in a Sorvall SS34 rotor. The aqueous phase was removed and placed in a 15 ml Falcon Tube. An equal volume of isopropanol was added and left at -20°C overnight. The precipitated RNA was spun down at $9,000 \text{ rpm}$ for 15 min in a Sorvall SS34 rotor and washed in 70% ethanol. The pellet was redissolved in $300 \mu\text{l}$ of RNase-free water and $35 \mu\text{l}$ buffer (Promega) $5 \mu\text{l}$ DTT, $7 \mu\text{l}$ RNasin and $8 \mu\text{l}$ DNase were added. The tube was incubated at 37°C for 30 minutes to remove contaminating genomic DNA, extracted once with phenol chloroform and re-precipitated with 1/10 volume of 3M sodium acetate and 2 volumes of 100% ethanol. The RNA was spun down and placed in RNase free water. RNA was stored at -80°C .

AI_comprehensive panel_v1.0

The plates for AI_comprehensive panel_v1.0 include two control wells and 89 test samples comprised of cDNA isolated from surgical and postmortem human tissues obtained from the Backus Hospital and Clinomics (Frederick, MD). Total RNA was extracted from tissue samples from the Backus Hospital in the Facility at CuraGen. Total RNA from other

Joint tissues including synovial fluid, synovium, bone and cartilage were obtained from patients undergoing total knee or hip replacement surgery at the Backus Hospital. Tissue samples were immediately snap frozen in liquid nitrogen to ensure that isolated RNA was of optimal quality and not degraded. Additional samples of osteoarthritis and rheumatoid arthritis joint tissues were obtained from Clinomics. Normal control tissues were supplied by Clinomics and were obtained during autopsy of trauma victims.

Surgical specimens of psoriatic tissues and adjacent matched tissues were provided as total RNA by Clinomics. Two male and two female patients were selected between the ages of 25 and 47. None of the patients were taking prescription drugs at the time samples were isolated.

Surgical specimens of diseased colon from patients with ulcerative colitis and Crohn's disease and adjacent matched tissues were obtained from Clinomics. Bowel tissue from three female and three male Crohn's patients between the ages of 41-69 were used. Two patients were not on prescription medication while the others were taking dexamethasone, phenobarbital, or tylenol. Ulcerative colitis tissue was from three male and four female patients. Four of the patients were taking lebid and two were on phenobarbital.

Total RNA from post mortem lung tissue from trauma victims with no disease or with emphysema, asthma or COPD was purchased from Clinomics. Emphysema patients ranged in age from 40-70 and all were smokers, this age range was chosen to focus on patients with cigarette-linked emphysema and to avoid those patients with alpha-1 anti-trypsin deficiencies. Asthma patients ranged in age from 36-75, and excluded smokers to prevent those patients that could also have COPD. COPD patients ranged in age from 35-80 and included both smokers and non-smokers. Most patients were taking corticosteroids, and bronchodilators.

In the labels employed to identify tissues in the AI_comprehensive panel_v1.0 panel, the following abbreviations are used:

AI = Autoimmunity
 Syn = Synovial
 Normal = No apparent disease
 OA = Osteoarthritis
 (SS) (BA) (MF) = Individual patients

Adj = Adjacent tissue
 Match control = adjacent tissues
 -M = Male
 -F = Female
 COPD = Chronic obstructive pulmonary disease

Panels 5D and 5I

The plates for Panel 5D and 5I include two control wells and a variety of cDNAs isolated from human tissues and cell lines with an emphasis on metabolic diseases. Metabolic tissues were obtained from patients enrolled in the Gestational Diabetes study. Cells were obtained during different stages in the differentiation of adipocytes from human mesenchymal stem cells. Human pancreatic islets were also obtained.

In the Gestational Diabetes study subjects are young (18 - 40 years), otherwise healthy women with and without gestational diabetes undergoing routine (elective) Caesarean section. After delivery of the infant, when the surgical incisions were being repaired/closed, the obstetrician removed a small sample (<1 cc) of the exposed metabolic tissues during the closure of each surgical level. The biopsy material was rinsed in sterile saline, blotted and fast frozen within 5 minutes from the time of removal. The tissue was then flash frozen in liquid nitrogen and stored, individually, in sterile screw-top tubes and kept on dry ice for shipment to or to be picked up by CuraGen. The metabolic tissues of interest include uterine wall (smooth muscle), visceral adipose, skeletal muscle (rectus) and subcutaneous adipose. Patient descriptions are as follows:

Patient 2	Diabetic Hispanic, overweight, not on insulin
Patient 7-9	Nondiabetic Caucasian and obese (BMI>30)
Patient 10	Diabetic Hispanic, overweight, on insulin
Patient 11	Nondiabetic African American and overweight
Patient 12	Diabetic Hispanic on insulin

Adipocyte differentiation was induced in donor progenitor cells obtained from Osirus (a division of Clonetics/BioWhittaker) in triplicate, except for Donor 3U which had only two replicates. Scientists at Clonetics isolated, grew and differentiated human mesenchymal stem cells (HuMSCs) for CuraGen based on the published protocol found in Mark F. Pittenger, et al. Multilineage Potential of Adult Human Mesenchymal Stem Cells Science Apr 2 1999.

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Donor 2 and 3 U: Mesenchymal Stem cells, Undifferentiated Adipose
Donor 2 and 3 AM: Adipose, AdiposeMidway Differentiated
Donor 2 and 3 AD: Adipose, Adipose Differentiated

Human cell lines were generally obtained from ATCC (American Type Culture Collection), NCI or the German tumor cell bank and fall into the following tissue groups: kidney proximal convoluted tubule, uterine smooth muscle cells, small intestine, liver HepG2 cancer cells, heart primary stromal cells, and adrenal cortical adenoma cells. These cells are all cultured under standard recommended conditions and RNA extracted using the standard procedures. All samples were processed at CuraGen to produce single stranded cDNA.

Panel 5I contains all samples previously described with the addition of pancreatic islets from a 58 year old female patient obtained from the Diabetes Research Institute at the University of Miami School of Medicine. Islet tissue was processed to total RNA at an outside source and delivered to CuraGen for addition to panel 5I.

In the labels employed to identify tissues in the 5D and 5I panels, the following abbreviations are used:

GO Adipose = Greater Omentum Adipose
SK = Skeletal Muscle
UT = Uterus
PL = Placenta
AD = Adipose Differentiated
AM = Adipose Midway Differentiated
U = Undifferentiated Stem Cells

Panel CNSD.01

The plates for Panel CNSD.01 include two control wells and 94 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard Brain Tissue Resource Center. Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

disease, Progressive Supranuclear Palsy, Depression, and "Normal controls". Within each of these brains, the following regions are represented: cingulate gyrus, temporal pole, globus

palladus, substantia nigra, Brodman Area 4 (primary motor strip), Brodman Area 7 (parietal cortex), Brodman Area 9 (prefrontal cortex), and Brodman area 17 (occipital cortex). Not all brain regions are represented in all cases; e.g., Huntington's disease is characterized in part by neurodegeneration in the globus palladus, thus this region is impossible to obtain from confirmed Huntington's cases. Likewise Parkinson's disease is characterized by degeneration of the substantia nigra making this region more difficult to obtain. Normal control brains were examined for neuropathology and found to be free of any pathology consistent with neurodegeneration.

In the labels employed to identify tissues in the CNS panel, the following abbreviations are used:

PSP = Progressive supranuclear palsy
Sub Nigra = Substantia nigra
Glob Palladus= Globus palladus
Temp Pole = Temporal pole
Cing Gyr = Cingulate gyrus
BA 4 = Brodman Area 4

Panel CNS_Neurodegeneration_V1.0

The plates for Panel CNS_Neurodegeneration_V1.0 include two control wells and 47 test samples comprised of cDNA isolated from postmortem human brain tissue obtained from the Harvard Brain Tissue Resource Center (McLean Hospital) and the Human Brain and Spinal Fluid Resource Center (VA Greater Los Angeles Healthcare System). Brains are removed from calvaria of donors between 4 and 24 hours after death, sectioned by neuroanatomists, and frozen at -80°C in liquid nitrogen vapor. All brains are sectioned and examined by neuropathologists to confirm diagnoses with clear associated neuropathology.

Disease diagnoses are taken from patient records. The panel contains six brains from Alzheimer's disease (AD) patients, and eight brains from "Normal controls" who showed no evidence of dementia prior to death. The eight normal control brains are divided into two categories: Controls with no dementia and no Alzheimer's like pathology (Controls) and controls with no dementia but evidence of severe Alzheimer's like pathology, (specifically

hippocampus, temporal cortex (Brodman area 21), parietal cortex (Brodman area 7), and occipital cortex (Brodman area 17). These regions were chosen to encompass all levels of

neurodegeneration in AD. The hippocampus is a region of early and severe neuronal loss in AD; the temporal cortex is known to show neurodegeneration in AD after the hippocampus; the parietal cortex shows moderate neuronal death in the late stages of the disease; the occipital cortex is spared in AD and therefore acts as a "control" region within AD patients. Not all brain regions are represented in all cases.

In the labels employed to identify tissues in the CNS_Neurodegeneration_V1.0 panel, the following abbreviations are used:

AD = Alzheimer's disease brain; patient was demented and showed AD-like pathology upon autopsy

Control = Control brains; patient not demented, showing no neuropathology

Control (Path) = Control brains; patient not demented but showing severe AD-like pathology

Sup Temporal Ctx = Superior Temporal Cortex

Inf Temporal Ctx = Inferior Temporal Cortex

A. CG58522-01: HUMAN PLATELET-ACTIVATING FACTOR ACETYLHYDROLASE IB BETA

Expression of gene CG58522-01 was assessed using the primer-probe set Ag3365, described in Table AA. Results of the RTQ-PCR runs are shown in Table AB.

Table AA. Probe Name Ag3365

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cagaatgaaccaaggagactca-3'	22	3	357
Probe	TET-5'-ctactccgcatgcccagaagacatt-3'-TAMRA	26	35	358
Reverse	5'-cacatccatctgtcatctcctt-3'	22	62	359

Table AB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3365, Run 216709759	Tissue Name	Rel. Exp.(%) Ag3365, Run 216709759
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(A).T	0.0	Colon ca. SW-948	0.0

LOXIMVI			
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	10.7	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	4.9	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	7.9	Stomach Pool	0.0
Ovarian ca. OVCAR-8	26.8	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	1.7	Lymph Node Pool	16.5
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	3.3	CNS cancer (astro) SF-75	0.0
		CNS	
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	25.7

Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	100.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	4.8
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	1.8
Liver	0.0	Brain (Thalamus) Pool	3.6
Fetal Liver	0.0	Brain (whole)	6.9
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3365 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3365 - Significant expression of this gene is seen only in the lung cancer cell line NCI-H23 (CT=33.1). Therefore, expression of this gene may be used to distinguish this sample from the other samples on this panel.

Panel 4D Summary: Ag3365 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

B. CG58520-01: GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1

Expression of gene CG58520-01 was assessed using the primer-probe set Ag3364, described in Table BA.

Table BA. Probe Name Ag3364

Primers	Sequences	Length	Start Position	SEQ ID NO:
Reverse	5'-tcattctgctttatctatcaggtttc-3'	22	106	362

CNS_neurodegeneration_v1.0 Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel CNS_1 Summary: Ag3364 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

C. CG58520-03: GAMMA-AMINOBUTYRIC-ACID RECEPTOR GAMMA-1 SUBUNIT PRECURSOR (GABA(A) RECEPTOR)

Expression of gene CG58520-03 was assessed using the primer-probe set Ag5092, described in Table CA.

Table CA. Probe Name Ag5092

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gaacattcctgtccactgga-3'	20	625	363
Probe	TET-5'-atTTTcaagcgatggataccctaaaa-3'- TAMRA	26	645	364
Reverse	5'-cacttctacggagggtttt-3'	20	692	365

CNS_neurodegeneration_v1.0 Summary: Ag5092 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.5 Summary: Ag5092 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4.1D Summary: Ag5092 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

D. CG58518-01: GAMMA-AMINOBUTYRIC ACID RECEPTOR RHO-3

Expression of gene CG58518-01 was assessed using the primer-probe sets Ag3363, Ag1130, Ag1198, Ag1253 and Ag1603, described in Tables DA, DB, DC, DD and DE. Results of the RTQ-PCR runs are shown in Tables DF, DG and DH.

Table DA. Probe Name Ag3363

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tggtttccagttagtctcctt-3'	22	14	366
Probe	TET-5'-cacctacatctggatcatattgaaacca-3'- TAMRA	28	36	367
Reverse	5'-ttgatgttagaagcagcacaaaa-3'	22	68	368

Table DB. Probe Name Ag1130

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtcctggctttccagttagtct-3'	22	10	369
Probe	TET-5'-tcacctacatctggatcatattgaaacca-3'- TAMRA	29	35	370
Reverse	5'-ttgatgttagaagcagcacaaaa-3'	22	68	371

Table DC. Probe Name Ag1198

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtcctggctttccagttagtct-3'	22	10	372
Probe	TET-5'-tcacctacatctggatcatattgaaacca-3'- TAMRA	29	35	373
Reverse	5'-ttgatgttagaagcagcacaaaa-3'	22	68	374

Table DD. Probe Name Ag1253

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atctgggtgcctgatattctttt-3'	22	466	375
Probe	TET-5'-tgtccactctaaaagatccttcatccatga-3'- TAMRA	30	489	376
Reverse	5'-cgcagcatgatattctccatag-3'	22	524	377

Primers	Sequences	Length	Start Position	SEQ ID NO:
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Forward	5'-gtcctggctttccagttagtct-3'	22	10	378
Probe	TET-5'-tcacctacatctggatcatattgaaacca-3'- TAMRA	29	35	379
Reverse	5'-ttgatgttagaagcagcacaaa-3'	22	68	380

Table DF. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3363, Run 216709559	Tissue Name	Rel. Exp.(%) Ag3363, Run 216709559
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	6.6
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	16.7	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV- 1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. BT-20	0.0	Fetal Skeletal Muscle	0.0

Breast ca. T47D	6.4	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	8.5
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	10.9
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	77.9	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	100.0	CNS cancer (glio) SF- 295	11.4
Lung ca. A549	10.1	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	34.4	Brain (fetal)	0.0
Lung ca. NCI-H460	30.6	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	5.1
Fetal Liver	0.0	Brain (whole)	50.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	3.0	Adrenal Gland	0.0
Fetal Kidney	8.4	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

Table DG. Panel 1.2

Tissue	Rel. Exp.(%) Ag1130.	Rel. Exp.(%) Ag1130.	Rel. Exp.(%) Ag1198.	Tissue	Rel. Exp.(%) Ag1130.	Rel. Exp.(%) Ag1130.	Rel. Exp.(%) Ag1198.
MDA-MB-231 cells				Renal ca. 786-0			

Heart (Fetal)	0.0	0.0	0.0	Renal ca. A498	7.3	4.7	0.0
Pancreas	0.0	0.0	0.0	Renal ca. RXF 393	0.0	0.0	0.0
Pancreatic ca. CAPAN 2	9.0	0.0	0.0	Renal ca. ACHN	0.0	0.0	0.0
Adrenal Gland	0.0	2.6	0.0	Renal ca. UO-31	3.9	0.0	0.0
Thyroid	0.0	0.0	0.0	Renal ca. TK-10	0.0	0.0	0.0
Salivary gland	0.0	0.0	0.0	Liver	26.6	0.0	0.0
Pituitary gland	0.0	0.0	0.0	Liver (fetal)	25.3	0.0	0.0
Brain (fetal)	0.0	0.0	0.0	Liver ca. (hepatoblast) HepG2	0.0	0.0	0.0
Brain (whole)	2.6	20.0	0.0	Lung	0.0	0.0	0.0
Brain (amygdala)	1.3	32.1	0.0	Lung (fetal)	0.0	0.0	0.0
Brain (cerebellum)	1.5	3.8	0.0	Lung ca. (small cell) LX-1	3.4	0.0	0.0
Brain (hippocampus)	0.0	27.0	0.0	Lung ca. (small cell) NCI-H69	28.5	74.2	0.0
Brain (thalamus)	9.9	22.5	9.8	Lung ca. (s.cell var.) SHP-77	3.8	9.7	0.0
Cerebral Cortex	0.0	0.0	0.0	Lung ca. (large cell)NCI-H460	8.8	4.1	5.3
Spinal cord	4.4	0.0	0.0	Lung ca. (non-sm. cell) A549	51.4	9.5	7.2
glio/astro U-87-MG	0.0	0.0	0.0	Lung ca. (non-s. cell)	0.0	0.0	0.0
glioblastoma U-118-MG				non-s. cell)			

				HOP-62			
astrocytoma SW1783	2.9	0.0	0.0	Lung ca. (non-s.cl) NCI-H522	0.0	0.0	0.0
neuro*; met SK-N-AS	0.0	0.0	0.0	Lung ca. (squam.) SW 900	3.2	8.7	0.0
astrocytoma SF-539	5.1	0.0	0.0	Lung ca. (squam.) NCI-H596	2.3	15.9	0.0
astrocytoma SNB-75	2.3	0.0	0.0	Mammary gland	0.0	0.0	0.0
glioma SNB-19	6.3	20.7	9.0	Breast ca.* (pl.ef) MCF-7	0.0	0.0	0.0
glioma U251	1.4	0.0	1.8	Breast ca.* (pl.ef) MDA-MB-231	0.0	0.0	0.0
glioma SF-295	0.0	0.0	0.0	Breast ca.* (pl.ef) T47D	14.1	37.4	0.0
Heart	0.0	0.0	0.0	Breast ca. BT-549	12.5	21.0	12.3
Skeletal Muscle	2.3	0.0	0.0	Breast ca. MDA-N	0.0	0.0	0.0
Bone marrow	0.0	0.0	0.0	Ovary	0.0	0.0	0.0
Thymus	0.0	0.0	0.0	Ovarian ca. OVCAR-3	0.0	0.0	0.0
Spleen	2.2	0.0	0.0	Ovarian ca. OVCAR-4	0.0	0.0	0.0
Lymph node	0.0	0.0	0.0	Ovarian ca. OVCAR-	66.9	35.4	4.4
ISSUE				OVCAR-			

				8			
Stomach	0.0	0.0	0.0	Ovarian ca. IGROV-1	6.0	0.0	0.0
Small intestine	5.4	0.0	0.0	Ovarian ca. (ascites) SK-OV-3	30.8	0.0	0.0
Colon ca. SW480	3.2	0.0	0.0	Uterus	0.0	0.0	0.0
Colon ca.* SW620 (SW480 met)	0.0	0.0	0.0	Placenta	0.0	0.0	0.0
Colon ca. HT29	1.9	14.4	0.0	Prostate	6.9	0.0	0.0
Colon ca. HCT-116	0.0	0.0	0.0	Prostate ca.* (bone met) PC-3	100.0	0.0	0.0
Colon ca. CaCo-2	0.0	0.0	0.0	Testis	54.7	100.0	36.9
Colon ca. Tissue (ODO3866)	72.2	75.8	100.0	Melanom a Hs688(A). T	4.2	0.0	0.0
Colon ca. HCC-2998	5.3	4.8	0.0	Melanom a* (met) Hs688(B). T	2.7	34.2	13.3
Gastric ca.* (liver met) NCI-N87	50.3	0.0	0.0	Melanom a UACC- 62	0.0	0.0	0.0
Bladder	6.0	22.1	0.0	Melanom a M14	31.4	36.3	20.2
Trachea	0.0	0.0	0.0	Melanom a LOX IMVI	0.0	0.0	0.0
Kidney	2.0	0.0	0.0	Melanom a* (met) SK-MEL- 5	2.4	0.0	0.0
Kidney (cell)	1.1	2.5	0.0				

Tissue Name	Rel. Exp.(%)	Tissue Name	Rel. Exp.(%)
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	Ag1198, Run 142014937		Ag1198, Run 142014937
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	2.5	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	16.4
LAK cells IL-2+IL-12	0.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
PMA ionomycin			
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0

Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti-CD40	0.0	IBD Colitis 1	100.0
Monocytes rest	0.0	IBD Colitis 2	0.0
Monocytes LPS	0.0	IBD Crohn's	0.0
Macrophages rest	0.0	Colon	0.0
Macrophages LPS	0.0	Lung	0.0
HUVEC none	0.0	Thymus	0.0
HUVEC starved	0.0	Kidney	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3363 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3363 - Significant expression is seen in lung cancer cell line NCI-H146 (CT=34.5) and lung cancer cell line SHP-77 (CT=34.2). Therefore, expression of this can be used to distinguish these samples from the rest of the samples on this panel.

Ag3363 Summary: Ag3363 - Significant expression is seen in lung cancer cell line NCI-H146 (CT=34.5) and lung cancer cell line SHP-77 (CT=34.2). Therefore, expression of this gene can be used to differentiate these samples

from other samples on these panels. Results from a third experiment using the probe and primer set Ag1253 show low/undetectable levels of expression in all the samples on this panel.

Panel 1.3D Summary: Agl253 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 2D Summary: Ag1603 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag1130/Ag1198/Ag1253/Ag3363 - Two experiments showed possible experimental difficulties, while the other three runs showed expression of this gene as low/undetectable (CTs > 35) across all of the samples on the panel.

Panel 4R Summary: Ag1198 - Significant expression of this gene is seen only in the IBD colitis 1 sample (CT=34.2). Therefore, expression of this gene can be used to differentiate this sample from others on the panel.

Panel CNS_1 Summary: Ag1253/Ag1603 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

E. CG58516-01: G-protein beta WD-40 repeats

Expression of gene CG58516-01 was assessed using the primer-probe set Ag3362, described in Table EA. Results of the RTQ-PCR runs are shown in Tables EB and EC.

Table EA. Probe Name Ag3362

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtcgggcaggaccttact-3'	19	1474	381
Probe	TET-5'-tcttacagctaattctgcagggcaca-3'-TAMRA	26	1498	382
Reverse	5'-tacgctttactcccgaagtca-3'	22	1543	383

Table EB. CNS neurodegeneration_v1.0

[illegible]

AD 2 Hippo	33.2	Control (Path) 4 Temporal Ctx	24.3
AD 3 Hippo	4.3	AD 1 Occipital Ctx	2.0
AD 4 Hippo	16.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	96.6	AD 3 Occipital Ctx	5.4
AD 6 Hippo	43.2	AD 4 Occipital Ctx	24.7
Control 2 Hippo	29.1	AD 5 Occipital Ctx	24.5
Control 4 Hippo	16.6	AD 6 Occipital Ctx	31.9
Control (Path) 3 Hippo	3.8	Control 1 Occipital Ctx	0.9
AD 1 Temporal Ctx	7.1	Control 2 Occipital Ctx	89.5
AD 2 Temporal Ctx	23.2	Control 3 Occipital Ctx	12.6
AD 3 Temporal Ctx	5.6	Control 4 Occipital Ctx	6.3
AD 4 Temporal Ctx	20.0	Control (Path) 1 Occipital Ctx	65.1
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	15.8
AD 5 Sup Temporal Ctx	43.8	Control (Path) 3 Occipital Ctx	2.0
AD 6 Inf Temporal Ctx	30.8	Control (Path) 4 Occipital Ctx	11.6
AD 6 Sup Temporal Ctx	69.7	Control 1 Parietal Ctx	2.8
Control 1 Temporal Ctx	9.0	Control 2 Parietal Ctx	39.2
Control 2 Temporal Ctx	59.0	Control 3 Parietal Ctx	23.5
Control 3 Temporal Ctx	11.7	Control (Path) 1 Parietal Ctx	69.7
Control 4 Temporal Ctx	8.2	Control (Path) 2 Parietal Ctx	14.9
Control (Path) 1 Temporal Ctx	56.3	Control (Path) 3 Parietal Ctx	0.9
Control (Path) 2 Temporal Ctx	34.2	Control (Path) 4 Parietal Ctx	38.7

Table EC. General screening panel v1.4

Issue Name	Run 216523482	Issue Name	Run 216523482
Adipose	6.3	Renal ca. TK-10	44.1

Melanoma* Hs688(A).T	17.6	Bladder	9.4
Melanoma* Hs688(B).T	18.3	Gastric ca. (liver met.) NCI-N87	21.6
Melanoma* M14	17.1	Gastric ca. KATO III	17.6
Melanoma* LOXIMVI	13.6	Colon ca. SW-948	5.8
Melanoma* SK- MEL-5	19.6	Colon ca. SW480	34.6
Squamous cell carcinoma SCC-4	14.6	Colon ca.* (SW480 met) SW620	14.2
Testis Pool	4.0	Colon ca. HT29	7.2
Prostate ca.* (bone met) PC-3	90.8	Colon ca. HCT-116	14.3
Prostate Pool	4.0	Colon ca. CaCo-2	19.8
Placenta	11.4	Colon cancer tissue	3.6
Uterus Pool	2.1	Colon ca. SW1116	9.4
Ovarian ca. OVCAR-3	17.4	Colon ca. Colo-205	8.8
Ovarian ca. SK-OV- 3	47.0	Colon ca. SW-48	13.2
Ovarian ca. OVCAR-4	14.7	Colon Pool	5.7
Ovarian ca. OVCAR-5	31.6	Small Intestine Pool	10.2
Ovarian ca. IGROV- 1	12.9	Stomach Pool	6.2
Ovarian ca. OVCAR-8	6.7	Bone Marrow Pool	1.3
Ovary	12.5	Fetal Heart	1.1
Breast ca. MCF-7	75.8	Heart Pool	3.4
Breast ca. MDA- MB-231	30.4	Lymph Node Pool	8.7
Breast ca. BT 549	65.5	Fetal Skeletal Muscle	2.3
Breast ca. T47D	100.0	Skeletal Muscle Pool	9.4
Breast ca. MDA-N	33.4	Spleen Pool	4.6
Breast Pool	4.6	Thymus Pool	7.3
Trachea	7.7	CNS cancer (glio/astro) U87-MG	33.9
Lung	4.9	CNS cancer (glio/astro) U87-MG	27.2
Lung ca. NCI-N417	9.3	CNS cancer (astro) SF- 539	14.3

Lung ca. LX-1	15.8	CNS cancer (astro) SNB-75	60.7
Lung ca. NCI-H146	4.9	CNS cancer (glio) SNB-19	13.8
Lung ca. SHP-77	16.5	CNS cancer (glio) SF- 295	28.5
Lung ca. A549	27.2	Brain (Amygdala) Pool	5.3
Lung ca. NCI-H526	4.1	Brain (cerebellum)	5.0
Lung ca. NCI-H23	15.0	Brain (fetal)	16.4
Lung ca. NCI-H460	9.5	Brain (Hippocampus) Pool	5.5
Lung ca. HOP-62	7.6	Cerebral Cortex Pool	8.7
Lung ca. NCI-H522	18.2	Brain (Substantia nigra) Pool	8.3
Liver	0.0	Brain (Thalamus) Pool	6.3
Fetal Liver	7.3	Brain (whole)	7.0
Liver ca. HepG2	29.5	Spinal Cord Pool	5.6
Kidney Pool	17.7	Adrenal Gland	6.3
Fetal Kidney	4.6	Pituitary gland Pool	0.8
Renal ca. 786-0	17.2	Salivary Gland	5.6
Renal ca. A498	5.1	Thyroid (female)	9.7
Renal ca. ACHN	17.3	Pancreatic ca. CAPAN2	11.7
Renal ca. UO-31	11.1	Pancreas Pool	9.2

CNS_neurodegeneration_v1.0 Summary: Ag3362 Highest expression of the CG58516-01 gene is seen in the occipital cortex of a control patient and the temporal cortex of an Alzheimer's patient. While the CG58516-01 gene does not appear to be preferentially expressed in Alzheimer's disease, this panel confirms expression of the CG58516-01 gene at moderate/high levels in the brain in an additional set of individuals. Please see Panel 1.4 for discussion of potential utility of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3362 The CG58516-01 gene is widely expressed in this panel, with highest expression in the breast cancer cell line T47D (CT=29). Significant expression is also seen in cell lines derived from prostate, breast and ovarian cancers. In general, expression of the CG58516-01 gene appears to be greater in the cancer cell lines than in normal tissue. Thus, the expression of this gene could be used to distinguish

low but significant levels in all brain regions examined. This gene encodes a protein with a

putative zinc-finger motif. Since these proteins are known to interact with nucleic acids, this suggests that this gene product may play a potential role in transcription. Thus, therapeutic modulation of the CG58516-01 gene product may be used to regulate the transcription of disease-related proteins such as ataxin, huntingtin, or various apoptosis cascade proteins.

Among tissues with metabolic function, this gene is expressed at low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, skeletal muscle, heart, and fetal liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

References:

1. Zhu W, Chan EK, Li J, Hemmerich P, Tan EM. (2001) Transcription activating property of autoantigen SG2NA and modulating effect of WD-40 repeats. *Exp Cell Res.* 269(2):312-21

Panel 4D Summary: Ag3362 Results from one experiment with the CG58516-01 gene are not included because the amp plot corresponding to the run indicates that there were problems with the experiment.

F. CG58473-01: PROTEIN KINASE

Expression of gene CG58473-01 was assessed using the primer-probe set Ag3357, described in Table FA. Results of the RTQ-PCR runs are shown in Tables FB and FC.

Table FA. Probe Name Ag3357

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtcaaggtggccctaaaattc-3'	21	853	384
Probe	TET-5'-ccaggacctcatctccaagctgctta-3'- TAMRA	26	897	385
Reverse	5'-agccgttctgaggggttat-3'	19	926	386

Table FB General screening panel v1.4

Tissue Name	REL EXP. OF AG3357 Run 216523477	Tissue Name	REL EXP. OF AG3357 Run 216523477
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Adipose	0.0	Renal ca. TK-10	13.2
Melanoma* Hs688(A).T	0.0	Bladder	7.2
Melanoma* Hs688(B).T	1.1	Gastric ca. (liver met.) NCI-N87	5.4
Melanoma* M14	50.0	Gastric ca. KATO III	49.0
Melanoma* LOXIMVI	33.0	Colon ca. SW-948	14.9
Melanoma* SK- MEL-5	24.7	Colon ca. SW480	95.9
Squamous cell carcinoma SCC-4	11.6	Colon ca.* (SW480 met) SW620	53.6
Testis Pool	8.2	Colon ca. HT29	10.3
Prostate ca.* (bone met) PC-3	3.2	Colon ca. HCT-116	76.3
Prostate Pool	0.0	Colon ca. CaCo-2	14.1
Placenta	2.4	Colon cancer tissue	6.3
Uterus Pool	0.0	Colon ca. SW1116	18.6
Ovarian ca. OVCAR-3	51.1	Colon ca. Colo-205	24.3
Ovarian ca. SK-OV- 3	53.2	Colon ca. SW-48	26.1
Ovarian ca. OVCAR-4	10.4	Colon Pool	4.6
Ovarian ca. OVCAR-5	12.3	Small Intestine Pool	1.7
Ovarian ca. IGROV- 1	10.1	Stomach Pool	1.2
Ovarian ca. OVCAR-8	13.4	Bone Marrow Pool	1.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	20.3	Heart Pool	0.0
Breast ca. MDA- MB-231	65.1	Lymph Node Pool	1.4
Breast ca. BT 549	100.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	34.2	Skeletal Muscle Pool	1.6
Breast ca. MDA-N	36.3	Spleen Pool	3.4
Breast Pool	1.3	Thymus Pool	4.7
Trachea	0.0	CNS cancer (glio/astro) U87-MG	7.8

Fetal Lung

 SS cancer
 (neuro/met) SK-N-AS

Lung ca. NCI-N417	17.9	CNS cancer (astro) SF-539	22.4
Lung ca. LX-1	28.5	CNS cancer (astro) SNB-75	19.2
Lung ca. NCI-H146	74.7	CNS cancer (glio) SNB-19	14.6
Lung ca. SHP-77	40.6	CNS cancer (glio) SF-295	3.0
Lung ca. A549	64.6	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	23.8	Brain (cerebellum)	0.0
Lung ca. NCI-H23	63.7	Brain (fetal)	0.0
Lung ca. NCI-H460	0.8	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	2.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	34.4	Brain (Substantia nigra) Pool	2.6
Liver	0.0	Brain (Thalamus) Pool	9.3
Fetal Liver	0.0	Brain (whole)	2.5
Liver ca. HepG2	11.4	Spinal Cord Pool	0.0
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	3.1	Pituitary gland Pool	1.4
Renal ca. 786-0	20.0	Salivary Gland	0.0
Renal ca. A498	3.6	Thyroid (female)	0.0
Renal ca. ACHN	18.9	Pancreatic ca. CAPAN2	20.4
Renal ca. UO-31	10.4	Pancreas Pool	1.3

Table FC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3357, Run 165231196	Tissue Name	Rel. Exp.(%) Ag3357, Run 165231196
Secondary Th1 act	9.0	HUVEC IL-1beta	9.5
Secondary Th2 act	43.2	HUVEC IFN gamma	6.3
Secondary Tr1 act	46.0	HUVEC TNF alpha + IFN gamma	7.3
Secondary Th1 rest	6.7	HUVEC TNF alpha + IL4	25.3
Secondary Th2 rest	12.2	HUVEC IL-11	13.1
Secondary Tr1 rest	1.9	Lung Microvascular EC none	3.3
		Lung Microvascular EC	
		none	
Primary Tr1 act	33.0	Microvascular Dermal EC	7.3

		TNFalpha + IL-1beta	
Primary Th1 rest	28.1	Bronchial epithelium TNFalpha + IL1beta	1.9
Primary Th2 rest	12.1	Small airway epithelium none	3.6
Primary Tr1 rest	29.7	Small airway epithelium TNFalpha + IL-1beta	36.3
CD45RA CD4 lymphocyte act	28.5	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	39.8	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	18.6	Astrocytes rest	1.4
Secondary CD8 lymphocyte rest	26.8	Astrocytes TNFalpha + IL-1beta	1.2
Secondary CD8 lymphocyte act	19.2	KU-812 (Basophil) rest	18.2
CD4 lymphocyte none	10.6	KU-812 (Basophil) PMA/ionomycin	30.4
2ry Th1/Th2/Tr1_anti- CD95 CH11	15.6	CCD1106 (Keratinocytes) none	18.3
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	7.7
LAK cells IL-2	42.6	Liver cirrhosis	25.7
LAK cells IL-2+IL-12	24.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	24.8	NCI-H292 none	7.8
LAK cells IL-2+ IL-18	40.3	NCI-H292 IL-4	26.4
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	29.7
NK Cells IL-2 rest	23.5	NCI-H292 IL-13	20.7
Two Way MLR 3 day	13.7	NCI-H292 IFN gamma	27.9
Two Way MLR 5 day	13.2	HPAEC none	8.6
Two Way MLR 7 day	11.7	HPAEC TNF alpha + IL-1 beta	2.4
PBMC rest	0.0	Lung fibroblast none	5.5
PBMC PWM	52.1	Lung fibroblast TNF alpha + IL-1 beta	2.2
PBMC PHA-L	14.6	Lung fibroblast IL-4	0.0
Ramos (B cell) none	16.5	Lung fibroblast IL-9	0.0
Ramos (B cell)	14.7	Lung fibroblast IL-13	0.0
		dermal fibroblast	
B lymphocytes CD40L and IL-4	10.4	Dermal fibroblast CCD1070 rest	40.1

EOL-1 dbcAMP	9.9	Dermal fibroblast CCD1070 TNF alpha	43.8
EOL-1 dbcAMP PMA/ionomycin	13.2	Dermal fibroblast CCD1070 IL-1 beta	23.5
Dendritic cells none	4.7	Dermal fibroblast IFN gamma	3.7
Dendritic cells LPS	1.1	Dermal fibroblast IL-4	4.6
Dendritic cells anti- CD40	0.0	IBD Colitis 2	0.0
Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	0.0	Colon	28.1
Macrophages rest	4.3	Lung	59.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	28.3	Kidney	10.0
HUVEC starved	25.3		

CNS_neurodegeneration_v1.0 Summary: Ag3357 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3357 This gene is primarily expressed in cancer cell lines, with highest expression in a breast cancer cell line BT 549(CT=32.8). This gene is expressed in the following cell lines but not the corresponding healthy tissue: gastric, brain, colon, lung, breast, ovarian cancer and melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

Panel 4D Summary: Ag3357 Highest expression of the CG58473-01 gene is seen in pokeweed mitogen-activated purified peripheral blood B lymphocytes (CT=33.2). In addition, no expression of the transcript is seen in PBMC that contain normal B cells, but the transcript is induced when PBMC are treated with the B cell selective pokeweed mitogen. The transcript is not seen in the B cell lymphoma cell line Ramos regardless of stimulation. Thus, the putative protein encoded by this gene could potentially be used diagnostically to identify activated B cells. Therefore, therapeutics that antagonize the function of this gene product may be useful as therapeutic drugs to reduce or eliminate the symptoms in patients with

colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

G. CG58470-01: UDP-N-ACETYLHEXOSAMINE PYROPHOSPHORYLASE

Expression of gene CG58470-01 was assessed using the primer-probe set Ag5940, described in Table GA.

Table GA. Probe Name Ag5940

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atatcctgaagctacaacagtttagct-3'	26	422	387
Probe	TET-5'-tggcaacaaatgcattattccatattacg-3'-TAMRA	29	459	388
Reverse	5'-gagtgaactcgctgggtcatg-3'	20	489	389

General_screening_panel_v1.5 Summary: Ag5940 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 5 Islet Summary: Ag5940 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

H. CG58593-01: UBIQUITIN-52

Expression of gene CG58593-01 was assessed using the primer-probe set Ag3421, described in Table HA.

Table HA. Probe Name Ag3421

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atctgctgcaagtgcctatgc-3'	20	291	390
Probe	TET-5'-cggtgctatcaactgccacaagaaga-3'-TAMRA	26	323	391
Reverse	5'-tgaccttcttctctggggtac-3'	20	371	392

CNS_neurodegeneration_v1.0 Summary: Ag3421 - Expression of this gene is

General_screening_panel_v1.4 Summary: Ag3421 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3421 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

I. CG57871-01: TOUSLED-LIKE KINASE

Expression of gene CG57871-01 was assessed using the primer-probe set Ag3351, described in Table IA. Results of the RTQ-PCR runs are shown in Tables IB and IC.

Table IA. Probe Name Ag3351

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gacccctcactgcaacattcttt-3'	22	346	393
Probe	TET-5'-aatcccttaccgacgagtagaaca-3'- TAMRA	26	372	394
Reverse	5'-gcactgccatctaaacctataga-3'	22	403	395

Table IB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3351, Run 210141594	Tissue Name	Rel. Exp.(%) Ag3351, Run 210141594
AD 1 Hippo	10.4	Control (Path) 3 Temporal Ctx	3.0
AD 2 Hippo	33.4	Control (Path) 4 Temporal Ctx	65.1
AD 3 Hippo	5.5	AD 1 Occipital Ctx	20.2
AD 4 Hippo	8.4	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	3.8
AD 6 Hippo	33.4	AD 4 Occipital Ctx	45.1
Control 2 Hippo	29.9	AD 5 Occipital Ctx	15.2
Control 4 Hippo	6.7	AD 6 Occipital Ctx	46.7
Control (Path) 3 Hippo	3.7	Control 1 Occipital Ctx	2.7
AD 1 Temporal Ctx	16.8	Control 2 Occipital Ctx	52.5
AD 2 Temporal Ctx	45.1	Control 3 Occipital Ctx	45.4
AD 3 Temporal Ctx	6.9	Control 4 Occipital Ctx	6.3
AD 5 Int Temporal Ctx	92.0	Control (Path) 2 Occipital Ctx	34.4

AD 5 Sup Temporal Ctx	13.0	Control (Path) 3 Occipital Ctx	0.8
AD 6 Inf Temporal Ctx	48.6	Control (Path) 4 Occipital Ctx	40.6
AD 6 Sup Temporal Ctx	56.6	Control 1 Parietal Ctx	6.9
Control 1 Temporal Ctx	6.2	Control 2 Parietal Ctx	48.0
Control 2 Temporal Ctx	29.3	Control 3 Parietal Ctx	26.1
Control 3 Temporal Ctx	32.8	Control (Path) 1 Parietal Ctx	73.7
Control 4 Temporal Ctx	13.9	Control (Path) 2 Parietal Ctx	57.4
Control (Path) 1 Temporal Ctx	79.6	Control (Path) 3 Parietal Ctx	3.4
Control (Path) 2 Temporal Ctx	97.3	Control (Path) 4 Parietal Ctx	78.5

Table IC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3351, Run 165222896	Tissue Name	Rel. Exp.(%) Ag3351, Run 165222896
Secondary Th1 act	16.5	HUVEC IL-1beta	15.4
Secondary Th2 act	26.4	HUVEC IFN gamma	13.5
Secondary Tr1 act	23.3	HUVEC TNF alpha + IFN gamma	17.0
Secondary Th1 rest	6.0	HUVEC TNF alpha + IL4	11.0
Secondary Th2 rest	10.7	HUVEC IL-11	5.4
Secondary Tr1 rest	2.1	Lung Microvascular EC none	12.4
Primary Th1 act	19.2	Lung Microvascular EC TNFalpha + IL-1beta	9.6
Primary Th2 act	17.6	Microvascular Dermal EC none	14.7
Primary Tr1 act	36.1	Microvascular Dermal EC TNFalpha + IL-1beta	14.8
Primary Th1 rest	55.5	Bronchial epithelium TNFalpha + IL1beta	14.1
		Small airway epithelium	

CD45RA CD4	13.0	Coronary artery SMC rest	15.6
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lymphocyte act			
CD45RO CD4 lymphocyte act	21.0	Coronary artery SMC TNFalpha + IL-1beta	6.1
CD8 lymphocyte act	12.9	Astrocytes rest	11.5
Secondary CD8 lymphocyte rest	14.9	Astrocytes TNFalpha + IL-1beta	11.8
Secondary CD8 lymphocyte act	14.8	KU-812 (Basophil) rest	19.2
CD4 lymphocyte none	10.7	KU-812 (Basophil) PMA/ionomycin	54.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	12.7	CCD1106 (Keratinocytes) none	12.2
LAK cells rest	17.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	9.0
LAK cells IL-2	22.4	Liver cirrhosis	7.4
LAK cells IL-2+IL-12	20.4	Lupus kidney	3.4
LAK cells IL-2+IFN gamma	37.9	NCI-H292 none	47.6
LAK cells IL-2+ IL-18	18.6	NCI-H292 IL-4	42.3
LAK cells PMA/ionomycin	10.5	NCI-H292 IL-9	30.4
NK Cells IL-2 rest	17.8	NCI-H292 IL-13	15.7
Two Way MLR 3 day	33.2	NCI-H292 IFN gamma	25.5
Two Way MLR 5 day	10.6	HPAEC none	13.5
Two Way MLR 7 day	9.9	HPAEC TNF alpha + IL-1 beta	17.7
PBMC rest	12.8	Lung fibroblast none	11.5
PBMC PWM	63.3	Lung fibroblast TNF alpha + IL-1 beta	12.4
PBMC PHA-L	18.0	Lung fibroblast IL-4	31.2
Ramos (B cell) none	14.0	Lung fibroblast IL-9	22.2
Ramos (B cell) ionomycin	77.9	Lung fibroblast IL-13	27.4
B lymphocytes PWM	100.0	Lung fibroblast IFN gamma	44.8
B lymphocytes CD40L and IL-4	30.8	Dermal fibroblast CCD1070 rest	33.7
EOL-1 dbcAMP	11.3	Dermal fibroblast CCD1070 TNF alpha	50.0
EOL-1 dbcAMP	13.7	Dermal fibroblast CCD1070 IL-1 beta	13.4
Dendritic cells LPS	19.8	Dermal fibroblast IL-4	25.7

Dendritic cells anti-CD40	14.2	IBD Colitis 2	2.0
Monocytes rest	22.5	IBD Crohn's	3.2
Monocytes LPS	32.8	Colon	26.8
Macrophages rest	31.0	Lung	14.6
Macrophages LPS	30.8	Thymus	28.7
HUVEC none	18.3	Kidney	45.4
HUVEC starved	45.7		

CNS_neurodegeneration_v1.0 Summary: Ag3351 - This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. While no differential expression of this gene is detected between Alzheimer's diseased postmortem brains and those of non-demented controls, the widespread expression of this gene in the brain suggests that therapeutic modulation of the expression or function of this gene may be effective in the treatment of neurologic disorders such as Parkinson's disease, epilepsy, stroke and multiple sclerosis.

General_screening_panel_v1.4 Summary: Ag3351 - Results from one experiment are not included. The amp plot indicates that there were experimental difficulties with this run.

Panel 4D Summary: Ag3351 The CG57871-01 gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

J. CG58590-01 and CG58590-02: PAI S Guanvlate kinase

probe set Ag3351, described in Table 1A. Results of the RT-PCR runs are shown in Table 1B.

JB, JC and JD. Please note that CG58590-02 represents a full-length physical clone of the CG58590-01 gene, validating the prediction of the gene sequence.

Table JA. Probe Name Ag3380

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tttgatacggcaattgtgaatt-3'	22	1931	396
Probe	TET-5'-ccgatcttgataaagcctatcaggaa-3'- TAMRA	26	1953	397
Reverse	5'-cccactgaggttcagtatcaag-3'	22	2000	398

Table JB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3380, Run 210153753	Tissue Name	Rel. Exp.(%) Ag3380, Run 210153753
AD 1 Hippo	12.9	Control (Path) 3 Temporal Ctx	4.7
AD 2 Hippo	27.7	Control (Path) 4 Temporal Ctx	24.3
AD 3 Hippo	4.8	AD 1 Occipital Ctx	15.6
AD 4 Hippo	7.7	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	100.0	AD 3 Occipital Ctx	7.5
AD 6 Hippo	64.2	AD 4 Occipital Ctx	19.1
Control 2 Hippo	25.5	AD 5 Occipital Ctx	29.5
Control 4 Hippo	9.9	AD 6 Occipital Ctx	40.1
Control (Path) 3 Hippo	8.4	Control 1 Occipital Ctx	4.2
AD 1 Temporal Ctx	17.6	Control 2 Occipital Ctx	65.5
AD 2 Temporal Ctx	25.3	Control 3 Occipital Ctx	13.4
AD 3 Temporal Ctx	4.9	Control 4 Occipital Ctx	6.4
AD 4 Temporal Ctx	17.4	Control (Path) 1 Occipital Ctx	78.5
AD 5 Inf Temporal Ctx	81.8	Control (Path) 2 Occipital Ctx	9.4
AD 5 SupTemporal	5.5	Control (Path) 3 Occipital Ctx	5.5
AD 6 Sup Temporal	53.6	Control 1 Parietal	6.0

Ctx		Ctx	
Control 1 Temporal Ctx	5.7	Control 2 Parietal Ctx	37.1
Control 2 Temporal Ctx	34.6	Control 3 Parietal Ctx	16.5
Control 3 Temporal Ctx	10.2	Control (Path) 1 Parietal Ctx	67.4
Control 4 Temporal Ctx	7.1	Control (Path) 2 Parietal Ctx	18.7
Control (Path) 1 Temporal Ctx	41.5	Control (Path) 3 Parietal Ctx	3.3
Control (Path) 2 Temporal Ctx	29.5	Control (Path) 4 Parietal Ctx	34.4

Table JC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3380, Run 217043276	Tissue Name	Rel. Exp.(%) Ag3380, Run 217043276
Adipose	9.0	Renal ca. TK-10	25.5
Melanoma* Hs688(A).T	18.9	Bladder	15.9
Melanoma* Hs688(B).T	16.8	Gastric ca. (liver met.) NCI-N87	52.5
Melanoma* M14	14.9	Gastric ca. KATO III	34.6
Melanoma* LOXIMVI	21.6	Colon ca. SW-948	4.9
Melanoma* SK-MEL-5	27.0	Colon ca. SW480	82.4
Squamous cell carcinoma SCC-4	28.7	Colon ca.* (SW480 met) SW620	20.6
Testis Pool	5.1	Colon ca. HT29	9.2
Prostate ca.* (bone met) PC-3	59.9	Colon ca. HCT-116	20.6
Prostate Pool	8.6	Colon ca. CaCo-2	22.8
Placenta	3.9	Colon cancer tissue	10.1
Uterus Pool	1.9	Colon ca. SW1116	6.2
Ovarian ca. OVCAR-3	32.5	Colon ca. Colo-205	4.9
Ovarian ca. SK-OV-3	57.4	Colon ca. SW-48	4.2

OVCAR-5		Small Intestine Caco-2	
Ovarian ca. IGROV-3	13.1	Stomach Pool	7.4

1			
Ovarian ca. OVCAR-8	19.2	Bone Marrow Pool	4.2
Ovary	5.9	Fetal Heart	6.3
Breast ca. MCF-7	35.1	Heart Pool	4.9
Breast ca. MDA-MB-231	58.2	Lymph Node Pool	11.4
Breast ca. BT 549	26.8	Fetal Skeletal Muscle	3.3
Breast ca. T47D	100.0	Skeletal Muscle Pool	8.1
Breast ca. MDA-N	8.7	Spleen Pool	5.6
Breast Pool	10.4	Thymus Pool	6.3
Trachea	5.5	CNS cancer (glio/astro) U87-MG	39.2
Lung	3.8	CNS cancer (glio/astro) U-118-MG	54.7
Fetal Lung	11.8	CNS cancer (neuro;met) SK-N-AS	19.6
Lung ca. NCI-N417	3.2	CNS cancer (astro) SF-539	12.2
Lung ca. LX-1	20.7	CNS cancer (astro) SNB-75	29.7
Lung ca. NCI-H146	3.8	CNS cancer (glio) SNB-19	13.4
Lung ca. SHP-77	17.9	CNS cancer (glio) SF-295	28.9
Lung ca. A549	30.6	Brain (Amygdala) Pool	11.8
Lung ca. NCI-H526	3.6	Brain (cerebellum)	6.0
Lung ca. NCI-H23	29.3	Brain (fetal)	8.4
Lung ca. NCI-H460	14.8	Brain (Hippocampus) Pool	14.5
Lung ca. HOP-62	19.5	Cerebral Cortex Pool	16.2
Lung ca. NCI-H522	28.7	Brain (Substantia nigra) Pool	16.0
Liver	0.4	Brain (Thalamus) Pool	22.7
Fetal Liver	11.9	Brain (whole)	5.9
Liver ca. HepG2	12.9	Spinal Cord Pool	16.0
Kidney Pool	18.4	Adrenal Gland	5.1
Fetal Kidney	22.8	Pituitary gland Pool	3.8
Renal ca. 786-0	28.5	Salivary Gland	2.1
Renal ca. A498	5.0	Thyroid (female)	8.2

Table JD, Panel 4D

Tissue Name	Rel. Exp.(%) Ag3380, Run 165296532	Tissue Name	Rel. Exp.(%) Ag3380, Run 165296532
Secondary Th1 act	13.1	HUVEC IL-1beta	15.0
Secondary Th2 act	14.6	HUVEC IFN gamma	19.6
Secondary Tr1 act	15.2	HUVEC TNF alpha + IFN gamma	28.3
Secondary Th1 rest	4.6	HUVEC TNF alpha + IL4	26.1
Secondary Th2 rest	4.7	HUVEC IL-11	7.8
Secondary Tr1 rest	8.0	Lung Microvascular EC none	25.5
Primary Th1 act	14.9	Lung Microvascular EC TNFalpha + IL-1beta	19.5
Primary Th2 act	13.2	Microvascular Dermal EC none	37.9
Primary Tr1 act	20.7	Microvascular Dermal EC TNFalpha + IL-1beta	24.8
Primary Th1 rest	35.6	Bronchial epithelium TNFalpha + IL1beta	37.1
Primary Th2 rest	24.0	Small airway epithelium none	15.0
Primary Tr1 rest	16.2	Small airway epithelium TNFalpha + IL-1beta	100.0
CD45RA CD4 lymphocyte act	23.3	Coronary artery SMC rest	30.1
CD45RO CD4 lymphocyte act	18.2	Coronary artery SMC TNFalpha + IL-1beta	13.6
CD8 lymphocyte act	7.4	Astrocytes rest	22.5
Secondary CD8 lymphocyte rest	13.4	Astrocytes TNFalpha + IL-1beta	21.2
Secondary CD8 lymphocyte act	4.4	KU-812 (Basophil) rest	17.9
CD4 lymphocyte none	8.0	KU-812 (Basophil) PMA/ionomycin	68.3
2ry Th1/Th2/Tr1_anti- CD95 CH11	10.7	CCD1106 (Keratinocytes) none	22.1
LAK cells rest	13.5	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	9.2
LAK cells IL-2	12.9	Liver cirrhosis	3.1
LAK cells IL-2+IL-12	13.2	Lupus kidney	2.9
LAK cells IL-2+IFN			
LAK cells PMA ionomycin	9.5	NCT-H292 IL-9	29.5

NK Cells IL-2 rest	7.0	NCI-H292 IL-13	36.6
Two Way MLR 3 day	15.2	NCI-H292 IFN gamma	42.6
Two Way MLR 5 day	7.0	HPAEC none	14.3
Two Way MLR 7 day	9.6	HPAEC TNF alpha + IL-1 beta	25.9
PBMC rest	6.4	Lung fibroblast none	12.5
PBMC PWM	60.7	Lung fibroblast TNF alpha + IL-1 beta	11.0
PBMC PHA-L	18.8	Lung fibroblast IL-4	25.9
Ramos (B cell) none	31.9	Lung fibroblast IL-9	20.6
Ramos (B cell) ionomycin	94.0	Lung fibroblast IL-13	18.8
B lymphocytes PWM	42.9	Lung fibroblast IFN gamma	23.3
B lymphocytes CD40L and IL-4	24.7	Dermal fibroblast CCD1070 rest	59.5
EOL-1 dbcAMP	12.9	Dermal fibroblast CCD1070 TNF alpha	64.2
EOL-1 dbcAMP PMA/ionomycin	10.4	Dermal fibroblast CCD1070 IL-1 beta	32.8
Dendritic cells none	19.6	Dermal fibroblast IFN gamma	10.7
Dendritic cells LPS	10.7	Dermal fibroblast IL-4	21.6
Dendritic cells anti-CD40	18.8	IBD Colitis 2	2.0
Monocytes rest	15.0	IBD Crohn's	3.6
Monocytes LPS	13.8	Colon	36.9
Macrophages rest	25.3	Lung	19.3
Macrophages LPS	8.1	Thymus	72.2
HUVEC none	19.9	Kidney	24.5
HUVEC starved	35.8		

CNS_neurodegeneration_v1.0 Summary: Ag3380 This panel does not show differential expression of the CG58590-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3380 - This gene is expressed at low to medium levels in all tissues in this system. The highest level of expression is seen in breast and prostate cancer cell lines. Available and prostate cancer cell lines are adenocarcinomas. The expression of this gene could be used as a diagnostic marker for the presence of these cancers.

Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and fetal liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes. Furthermore, this gene is more highly expressed in fetal (CT=30.9) liver when compared to expression in the adult (CT>35) and may be useful for the differentiation of the fetal and adult sources of this tissue.

In addition, this gene is expressed at moderate levels in the all regions of the CNS examined. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3380 - This gene is expressed from moderate to low levels across all of the samples on this panel. The highest expression is seen in small airway epithelium treated with TNFalpha and IL-1beta (CT=28.7). Interestingly, expression is much lower in untreated small airway epithelium (CT=31.5). There is also a significant difference between mononuclear cells treated with PWM (CT=29.5) and untreated cells (CT=32.7). Therefore, expression of this gene can be used to differentiate treated and untreated samples.

Expression of this gene is detected at a moderate level (CT=30.2) in normal colon (similar levels for colon are seen on panel 1.4 (CT=30.9), but is significantly lower in the IBD Colitis 2 (CT=34.4) and IBD Crohn's (CT=33.5) samples. Therefore, therapies designed with the protein encoded for by this gene may potentially modulate colon function and play a role in the identification and treatment of inflammatory or autoimmune diseases which effect the colon including Crohn's disease and ulcerative colitis.

K. CG58572-01 and CG58572-02: GLUCOSAMINE-PHOSPHATE N-ACETYLTRANSFERASE

in Tables KB, KC and KD

Table KA. Probe Name Ag3375

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -aagaagtggactggagtcagaa-3'	22	58	399
Probe	TET-5' -tacattttctccagccatttccccaa-3' - TAMRA	26	86	400
Reverse	5' -agcagtacaaagaggcctcaa-3'	21	135	401

Table KB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3375, Run 210154239	Tissue Name	Rel. Exp.(%) Ag3375, Run 210154239
AD 1 Hippo	17.1	Control (Path) 3 Temporal Ctx	4.8
AD 2 Hippo	19.3	Control (Path) 4 Temporal Ctx	27.5
AD 3 Hippo	7.4	AD 1 Occipital Ctx	11.5
AD 4 Hippo	4.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	72.2	AD 3 Occipital Ctx	5.9
AD 6 Hippo	53.6	AD 4 Occipital Ctx	12.7
Control 2 Hippo	20.3	AD 5 Occipital Ctx	26.6
Control 4 Hippo	6.8	AD 6 Occipital Ctx	19.8
Control (Path) 3 Hippo	5.5	Control 1 Occipital Ctx	3.2
AD 1 Temporal Ctx	11.6	Control 2 Occipital Ctx	36.1
AD 2 Temporal Ctx	23.8	Control 3 Occipital Ctx	7.4
AD 3 Temporal Ctx	5.5	Control 4 Occipital Ctx	4.1
AD 4 Temporal Ctx	16.5	Control (Path) 1 Occipital Ctx	66.0
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	8.2
AD 5 Sup Temporal Ctx	55.9	Control (Path) 3 Occipital Ctx	1.9
AD 6 Inf Temporal Ctx	37.9	Control (Path) 4 Occipital Ctx	12.2
AD 6 Sup Temporal Ctx	25.3	Control 1 Parietal	11.7
AD 6 Inf Parietal	25.3	Control 2 Parietal	11.7
AD 6 Sup Parietal	25.3	Control 3 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 4 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 5 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 6 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 7 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 8 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 9 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 10 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 11 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 12 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 13 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 14 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 15 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 16 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 17 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 18 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 19 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 20 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 21 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 22 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 23 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 24 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 25 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 26 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 27 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 28 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 29 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 30 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 31 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 32 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 33 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 34 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 35 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 36 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 37 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 38 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 39 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 40 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 41 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 42 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 43 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 44 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 45 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 46 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 47 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 48 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 49 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 50 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 51 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 52 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 53 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 54 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 55 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 56 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 57 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 58 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 59 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 60 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 61 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 62 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 63 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 64 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 65 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 66 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 67 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 68 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 69 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 70 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 71 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 72 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 73 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 74 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 75 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 76 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 77 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 78 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 79 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 80 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 81 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 82 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 83 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 84 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 85 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 86 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 87 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 88 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 89 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 90 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 91 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 92 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 93 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 94 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 95 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 96 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 97 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 98 Parietal	11.7
AD 6 Sup Occipital	25.3	Control 99 Parietal	11.7
AD 6 Inf Occipital	25.3	Control 100 Parietal	11.7

Ctx		Ctx	
Control 3 Temporal Ctx	8.2	Control (Path) 1 Parietal Ctx	49.7
Control 3 Temporal Ctx	4.0	Control (Path) 2 Parietal Ctx	15.4
Control (Path) 1 Temporal Ctx	52.9	Control (Path) 3 Parietal Ctx	4.2
Control (Path) 2 Temporal Ctx	26.6	Control (Path) 4 Parietal Ctx	32.5

Table KC. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3375, Run 165674233	Tissue Name	Rel. Exp.(%) Ag3375, Run 165674233
Liver adenocarcinoma	51.8	Kidney (fetal)	9.7
Pancreas	9.3	Renal ca. 786-0	19.6
Pancreatic ca. CAPAN 2	52.1	Renal ca. A498	26.2
Adrenal gland	8.9	Renal ca. RXF 393	15.7
Thyroid	6.3	Renal ca. ACHN	8.2
Salivary gland	18.3	Renal ca. UO-31	35.4
Pituitary gland	15.1	Renal ca. TK-10	9.8
Brain (fetal)	15.5	Liver	20.4
Brain (whole)	34.6	Liver (fetal)	16.5
Brain (amygdala)	16.0	Liver ca. (hepatoblast) HepG2	49.0
Brain (cerebellum)	34.2	Lung	4.5
Brain (hippocampus)	12.1	Lung (fetal)	5.4
Brain (substantia nigra)	12.8	Lung ca. (small cell) LX-1	32.3
Brain (thalamus)	17.9	Lung ca. (small cell) NCI-H69	17.3
Cerebral Cortex	10.4	Lung ca. (s.cell var.) SHP-77	30.1
Spinal cord	13.3	Lung ca. (large cell) NCI-H460	66.4
glio/astro U87-MG	14.8	Lung ca. (non-sm. cell) A549	19.1
glio/astro U-118-MG	95.3	Lung ca. (non-s.cell) NCI-H23	13.8

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LUNG CA. (small cell)
NCI-H522

Astrocytoma SF-539	11.4	Lung ca. (squam.) SW 900	9.9
Astrocytoma SNB-75	15.6	Lung ca. (squam.) NCI-H596	19.6
glioma SNB-19	11.8	Mammary gland	14.6
glioma U251	40.9	Breast ca.* (pl.ef) MCF-7	81.2
glioma SF-295	10.1	Breast ca.* (pl.ef) MDA-MB-231	91.4
Heart (fetal)	1.3	Breast ca.* (pl.ef) T47D	35.4
Heart	4.7	Breast ca. BT-549	97.9
Skeletal muscle (fetal)	1.2	Breast ca. MDA-N	14.8
Skeletal muscle	38.7	Ovary	1.6
Bone marrow	4.6	Ovarian ca. OVCAR-3	39.2
Thymus	2.7	Ovarian ca. OVCAR-4	23.0
Spleen	7.9	Ovarian ca. OVCAR-5	13.8
Lymph node	13.0	Ovarian ca. OVCAR-8	8.5
Colorectal	3.3	Ovarian ca. IGROV-1	5.6
Stomach	27.7	Ovarian ca.* (ascites) SK-OV-3	44.8
Small intestine	19.3	Uterus	19.5
Colon ca. SW480	16.5	Placenta	2.6
Colon ca.* SW620(SW480 met)	29.1	Prostate	15.6
Colon ca. HT29	13.8	Prostate ca.* (bone met)PC-3	56.6
Colon ca. HCT-116	27.7	Testis	40.6
Colon ca. CaCo-2	17.4	Melanoma Hs688(A).T	5.5
Colon ca. tissue(ODO3866)	26.4	Melanoma* (met) Hs688(B).T	8.9
Colon ca. HCC-2998	32.1	Melanoma UACC-62	17.8
Gastric ca.* (liver met) NCI-N87	100.0	Melanoma M14	27.7
		Melanoma LOX	
		SK-MEL-1	
Kidney	9.0	Adipose	8.0

Table KD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3375, Run 165296547	Tissue Name	Rel. Exp.(%) Ag3375, Run 165296547
Secondary Th1 act	14.6	HUVEC IL-1beta	24.5
Secondary Th2 act	13.0	HUVEC IFN gamma	24.5
Secondary Tr1 act	17.3	HUVEC TNF alpha + IFN gamma	24.0
Secondary Th1 rest	0.9	HUVEC TNF alpha + IL4	23.2
Secondary Th2 rest	1.5	HUVEC IL-11	12.1
Secondary Tr1 rest	2.9	Lung Microvascular EC none	21.3
Primary Th1 act	16.0	Lung Microvascular EC TNFalpha + IL-1beta	24.1
Primary Th2 act	12.1	Microvascular Dermal EC none	27.4
Primary Tr1 act	25.0	Microvascular Dermal EC TNFalpha + IL-1beta	24.0
Primary Th1 rest	10.4	Bronchial epithelium TNFalpha + IL1beta	20.3
Primary Th2 rest	6.1	Small airway epithelium none	11.3
Primary Tr1 rest	9.0	Small airway epithelium TNFalpha + IL-1beta	54.0
CD45RA CD4 lymphocyte act	14.6	Coronary artery SMC rest	23.5
CD45RO CD4 lymphocyte act	13.6	Coronary artery SMC TNFalpha + IL-1beta	12.0
CD8 lymphocyte act	14.2	Astrocytes rest	5.3
Secondary CD8 lymphocyte rest	14.4	Astrocytes TNFalpha + IL-1beta	5.4
Secondary CD8 lymphocyte act	5.8	KU-812 (Basophil) rest	19.5
CD4 lymphocyte none	2.4	KU-812 (Basophil) PMA/ionomycin	56.3
2ry Th1/Th2/Tr1_anti- CD95 CH11	2.6	CCD1106 (Keratinocytes) none	26.6
LAK cells rest	5.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	7.8
LAK cells IL-2	10.7	Liver cirrhosis	2.6
LAK cells IL-2 + IL-18	16.6	NCI-H292 IL-4	54.7

LAK cells PMA/ionomycin	12.5	NCI-H292 IL-9	45.7
NK Cells IL-2 rest	7.1	NCI-H292 IL-13	24.3
Two Way MLR 3 day	6.8	NCI-H292 IFN gamma	33.2
Two Way MLR 5 day	8.9	HPAEC none	17.8
Two Way MLR 7 day	6.0	HPAEC TNF alpha + IL-1 beta	30.1
PBMC rest	0.8	Lung fibroblast none	10.2
PBMC PWM	42.3	Lung fibroblast TNF alpha + IL-1 beta	6.3
PBMC PHA-L	11.6	Lung fibroblast IL-4	27.2
Ramos (B cell) none	30.6	Lung fibroblast IL-9	26.8
Ramos (B cell) ionomycin	100.0	Lung fibroblast IL-13	21.8
B lymphocytes PWM	77.4	Lung fibroblast IFN gamma	29.5
B lymphocytes CD40L and IL-4	12.2	Dermal fibroblast CCD1070 rest	42.3
EOL-1 dbcAMP	13.0	Dermal fibroblast CCD1070 TNF alpha	51.4
EOL-1 dbcAMP PMA/ionomycin	6.9	Dermal fibroblast CCD1070 IL-1 beta	22.5
Dendritic cells none	4.5	Dermal fibroblast IFN gamma	11.1
Dendritic cells LPS	3.8	Dermal fibroblast IL-4	19.5
Dendritic cells anti- CD40	2.9	IBD Colitis 2	0.7
Monocytes rest	2.2	IBD Crohn's	0.9
Monocytes LPS	1.3	Colon	7.6
Macrophages rest	6.6	Lung	6.2
Macrophages LPS	2.7	Thymus	9.4
HUVEC none	17.4	Kidney	4.2
HUVEC starved	37.4		

CNS_neurodegeneration_v1.0 Summary: Ag3375 This panel does not show differential expression of the CG58572-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

(C1-28.8). Based on expression in this panel, this gene may be involved in gastric, pancreatic,

brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene is expressed at moderate levels in the CNS. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3375 The CG58572-01 gene is ubiquitously expressed on this panel, with highest expression in the B cell line Ramos treated with ionomycin (CT=26.2). Significant levels of expression are also seen in pokeweed mitogen-activated B lymphocytes. Therefore, therapies that antagonize the function of this gene product may be useful as therapeutic drugs to reduce or eliminate the symptoms in patients with autoimmune and inflammatory diseases in which B cells play a part in the initiation or progression of the disease process, such as lupus erythematosus, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

Interestingly, there is a difference between the levels of expression in resting and activated secondary T cells. The level in activated secondary T cells (CT=28.7-29.2) appears to be higher than in resting T cells (CT=31.3-33.1). Therefore, therapeutics designed with the protein encoded by this transcript could be important in the regulation of T cell function.

L. CG58564-01 and CG58564-02: PROTEIN TYROSINE PHOSPHATASE -

Expression of gene CG58564-01 and full length clone CG58564-02 was assessed using the primer-probe sets Ag3023 and Ag3373, described in Tables LA and LB. Results of the

Table LA: Probe Name: Ag3023

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctaagtctggatttgccatca-3'	22	492	402
Probe	TET-5'-tcaggaatatgaagccatctacctagca-3'-TAMRA	28	517	403
Reverse	5'-tggagtgggtgacatcatctgta-3'	22	555	404

Table LB. Probe Name Ag3373

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atttgccatcaacttcaggaa-3'	22	502	405
Probe	TET-5'-tgaagccatctacctagcaaaattaaca-3'-TAMRA	28	526	406
Reverse	5'-tggagtgggtgacatcatctgta-3'	22	555	407

Table LC. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071	Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071
AD 1 Hippo	10.9	16.8	Control (Path) 3 Temporal Ctx	9.1	8.0
AD 2 Hippo	34.2	37.6	Control (Path) 4 Temporal Ctx	40.6	65.5
AD 3 Hippo	12.0	15.8	AD 1 Occipital Ctx	24.7	29.1
AD 4 Hippo	13.8	10.3	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	60.7	57.8	AD 3 Occipital Ctx	14.7	15.0
AD 6 Hippo	80.7	72.2	AD 4 Occipital Ctx	35.4	22.4

Control 4	10.9	16.8	AD 6	40.6	65.5
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Hippo			Occipital Ctx		
Control (Path) 3 Hippo	13.1	15.4	Control 1 Occipital Ctx	9.9	10.7
AD 1 Temporal Ctx	39.0	31.4	Control 2 Occipital Ctx	39.0	38.4
AD 2 Temporal Ctx	38.7	73.2	Control 3 Occipital Ctx	23.0	20.6
AD 3 Temporal Ctx	9.5	13.2	Control 4 Occipital Ctx	13.3	13.3
AD 4 Temporal Ctx	27.9	34.9	Control (Path) 1 Occipital Ctx	80.1	76.3
AD 5 Inf Temporal Ctx	59.0	100.0	Control (Path) 2 Occipital Ctx	17.3	20.0
AD 5 Sup Temporal Ctx	33.2	44.1	Control (Path) 3 Occipital Ctx	8.4	8.7
AD 6 Inf Temporal Ctx	100.0	73.2	Control (Path) 4 Occipital Ctx	21.2	20.6
AD 6 Sup Temporal Ctx	79.6	80.1	Control 1 Parietal Ctx	12.1	16.3
Control 1 Temporal Ctx	10.2	13.7	Control 2 Parietal Ctx	48.0	40.9
Control 2 Temporal Ctx	41.2	31.9	Control 3 Parietal Ctx	17.9	16.3
Control 3 Temporal Ctx	20.3	20.0	Control (Path) 1 Parietal Ctx	74.7	64.2
Control 4 Temporal Ctx	9.7	9.9	Control (Path) 2 Parietal Ctx	28.9	59.9
			Control		
Control (Path) 2 Temporal Ctx	44.2	44.2	Control (Path) 4	44.2	44.2

			Parietal Ctx		
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Table LD. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119	Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119
Adipose	12.0	Renal ca. TK-10	20.3
Melanoma* Hs688(A).T	30.8	Bladder	23.2
Melanoma* Hs688(B).T	69.3	Gastric ca. (liver met.) NCI-N87	25.3
Melanoma* M14	15.0	Gastric ca. KATO III	30.8
Melanoma* LOXIMVI	26.6	Colon ca. SW-948	9.7
Melanoma* SK- MEL-5	21.5	Colon ca. SW480	35.1
Squamous cell carcinoma SCC-4	33.0	Colon ca.* (SW480 met) SW620	13.9
Testis Pool	19.8	Colon ca. HT29	8.5
Prostate ca.* (bone met) PC-3	100.0	Colon ca. HCT-116	36.9
Prostate Pool	9.2	Colon ca. CaCo-2	42.9
Placenta	3.8	Colon cancer tissue	9.0
Uterus Pool	7.4	Colon ca. SW1116	5.8
Ovarian ca. OVCAR-3	28.5	Colon ca. Colo-205	4.3
Ovarian ca. SK-OV- 3	40.3	Colon ca. SW-48	4.2
Ovarian ca. OVCAR-4	20.0	Colon Pool	20.7
Ovarian ca. OVCAR-5	35.1	Small Intestine Pool	12.2
Ovarian ca. IGROV- 1	10.9	Stomach Pool	9.9
Ovarian ca. OVCAR-8	9.2	Bone Marrow Pool	11.6
Ovary	9.7	Fetal Heart	20.7
Breast ca. MCF-7	37.6	Heart Pool	10.6
Breast ca. MDA- MB-231	37.1	Lymph Node Pool	17.9
Breast ca. MDA-MB-231	17.3	Spleen Pool	17.3
Breast Pool	17.3	Thymus Pool	12.2

Trachea	12.0	CNS cancer (glio/astro) U87-MG	29.1
Lung	6.7	CNS cancer (glio/astro) U-118-MG	69.3
Fetal Lung	34.2	CNS cancer (neuro;met) SK-N-AS	34.9
Lung ca. NCI-N417	5.4	CNS cancer (astro) SF- 539	19.1
Lung ca. LX-1	17.2	CNS cancer (astro) SNB-75	35.8
Lung ca. NCI-H146	3.0	CNS cancer (glio) SNB-19	11.3
Lung ca. SHP-77	18.6	CNS cancer (glio) SF- 295	26.4
Lung ca. A549	29.1	Brain (Amygdala) Pool	4.5
Lung ca. NCI-H526	4.6	Brain (cerebellum)	8.1
Lung ca. NCI-H23	31.6	Brain (fetal)	13.2
Lung ca. NCI-H460	18.2	Brain (Hippocampus) Pool	5.3
Lung ca. HOP-62	14.1	Cerebral Cortex Pool	5.4
Lung ca. NCI-H522	31.6	Brain (Substantia nigra) Pool	4.8
Liver	1.2	Brain (Thalamus) Pool	8.0
Fetal Liver	32.3	Brain (whole)	6.2
Liver ca. HepG2	14.6	Spinal Cord Pool	6.6
Kidney Pool	22.1	Adrenal Gland	8.1
Fetal Kidney	26.1	Pituitary gland Pool	3.0
Renal ca. 786-0	28.7	Salivary Gland	4.7
Renal ca. A498	11.3	Thyroid (female)	4.4
Renal ca. ACHN	12.2	Pancreatic ca. CAPAN2	17.3
Renal ca. UO-31	24.1	Pancreas Pool	17.1

Table LE. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3023, Run 167966931	Tissue Name	Rel. Exp.(%) Ag3023, Run 167966931
Liver adenocarcinoma	51.1	Kidney (fetal)	26.2
Pancreas	6.1	Renal ca. 786-0	34.2
Pancreatic ca. CAPAN 2	17.7	Renal ca. A498	17.6

Salivary gland

Renal ca. UO-31

Pituitary gland	3.6	Renal ca. TK-10	23.0
Brain (fetal)	8.1	Liver	11.7
Brain (whole)	8.5	Liver (fetal)	8.0
Brain (amygdala)	6.7	Liver ca. (hepatoblast) HepG2	26.2
Brain (cerebellum)	15.2	Lung	3.1
Brain (hippocampus)	5.4	Lung (fetal)	11.0
Brain (substantia nigra)	9.0	Lung ca. (small cell) LX-1	12.9
Brain (thalamus)	4.2	Lung ca. (small cell) NCI-H69	9.9
Cerebral Cortex	2.0	Lung ca. (s.cell var.) SHP-77	67.8
Spinal cord	6.9	Lung ca. (large cell)NCI-H460	3.4
glio/astro U87-MG	28.5	Lung ca. (non-sm. cell) A549	45.1
glio/astro U-118-MG	46.7	Lung ca. (non-s.cell) NCI-H23	22.7
astrocytoma SW1783	40.6	Lung ca. (non-s.cell) HOP-62	25.7
neuro*; met SK-N-AS	27.2	Lung ca. (non-s.cl) NCI-H522	38.2
astrocytoma SF-539	29.7	Lung ca. (squam.) SW 900	27.4
astrocytoma SNB-75	35.1	Lung ca. (squam.) NCI-H596	29.9
glioma SNB-19	15.6	Mammary gland	5.1
glioma U251	37.9	Breast ca.* (pl.ef) MCF-7	47.0
glioma SF-295	18.4	Breast ca.* (pl.ef) MDA-MB-231	22.7
Heart (fetal)	2.9	Breast ca.* (pl.ef) T47D	86.5
Heart	12.9	Breast ca. BT-549	15.9
Skeletal muscle (fetal)	3.4	Breast ca. MDA-N	10.4
Skeletal muscle	36.3	Ovary	2.9
Bone marrow	4.5	Ovarian ca. OVCAR- 3	26.1
Thymus	14.3	Ovarian ca. OVCAR- 4	16.3
Lymph node	11.8	Ovarian ca. OVCAR- 8	9.5

Colorectal	10.4	Ovarian ca. IGROV-1	12.0
Stomach	7.8	Ovarian ca.* (ascites) SK-OV-3	100.0
Small intestine	5.1	Uterus	4.9
Colon ca. SW480	19.3	Placenta	1.3
Colon ca.* SW620(SW480 met)	42.9	Prostate	3.9
Colon ca. HT29	9.9	Prostate ca.* (bone met)PC-3	78.5
Colon ca. HCT-116	26.2	Testis	9.7
Colon ca. CaCo-2	41.5	Melanoma Hs688(A).T	5.9
Colon ca. tissue(ODO3866)	6.3	Melanoma* (met) Hs688(B).T	14.2
Colon ca. HCC-2998	16.0	Melanoma UACC-62	14.0
Gastric ca.* (liver met) NCI-N87	18.8	Melanoma M14	5.7
Bladder	30.6	Melanoma LOX IMVI	8.8
Trachea	3.2	Melanoma* (met) SK-MEL-5	14.7
Kidney	9.6	Adipose	18.9

Table LE. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3023, Run 164516146	Rel. Exp.(%) Ag3373, Run 165296617	Tissue Name	Rel. Exp.(%) Ag3023, Run 164516146	Rel. Exp.(%) Ag3373, Run 165296617
Secondary Th1 act	18.6	17.9	HUVEC IL-1beta	20.3	18.6
Secondary Th2 act	24.3	28.5	HUVEC IFN gamma	25.3	22.7
Secondary Tr1 act	22.8	21.8	HUVEC TNF alpha + IFN gamma	16.3	18.0
Secondary Th1 rest	7.5	6.8	HUVEC TNF alpha + IL4	18.2	13.4
Secondary Th2 rest	11.6	9.5	HUVEC IL-11	13.7	9.9
			Lung		
			Microvascular EC		

			TNFalpha + IL-1beta		
Primary Th2 act	20.2	19.3	Microvascular Dermal EC none	27.5	21.3
Primary Tr1 act	23.3	27.7	Microvascular Dermal EC TNFalpha + IL-1beta	20.7	19.9
Primary Th1 rest	51.1	51.4	Bronchial epithelium TNFalpha + IL1beta	13.0	16.3
Primary Th2 rest	26.2	29.5	Small airway epithelium none	8.1	8.5
Primary Tr1 rest	23.7	26.1	Small airway epithelium TNFalpha + IL-1beta	50.3	39.8
CD45RA CD4 lymphocyte act	14.6	11.0	Coronary artery SMC rest	20.2	18.9
CD45RO CD4 lymphocyte act	25.2	22.4	Coronary artery SMC TNFalpha + IL-1beta	12.0	9.8
CD8 lymphocyte act	20.4	15.8	Astrocytes rest	10.4	11.1
Secondary CD8 lymphocyte rest	16.5	19.9	Astrocytes TNFalpha + IL-1beta	11.7	9.8
Secondary CD8 lymphocyte act	13.2	9.3	KU-812 (Basophil) rest	47.6	38.2
CD4 lymphocyte none	17.1	11.6	KU-812 (Basophil) PMA/ionomycin	94.0	92.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	18.3	16.6	CCD1106 (Keratinocytes) none	19.9	13.2
LAK cells rest	25.5	16.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	6.0	4.8
LAK cells IL-2	27.2	22.5	Liver cirrhosis	3.1	2.7
LAK cells IL-2+IL-12	27.2	19.3	Lupus kidney	2.1	1.7
LAK cells IL-2 IL-18	35.1	29.7	NCI-H292 IL-4	33.9	34.0

LAK cells PMA/ionomycin	12.4	11.0	NCI-H292 IL-9	40.1	29.1
NK Cells IL-2 rest	20.0	15.0	NCI-H292 IL-13	16.2	14.2
Two Way MLR 3 day	24.0	16.7	NCI-H292 IFN gamma	16.6	18.4
Two Way MLR 5 day	12.9	10.1	HPAEC none	13.6	13.5
Two Way MLR 7 day	11.4	9.5	HPAEC TNF alpha + IL-1 beta	25.3	25.3
PBMC rest	13.7	10.5	Lung fibroblast none	11.4	14.2
PBMC PWM	69.3	66.4	Lung fibroblast TNF alpha + IL-1 beta	6.1	7.2
PBMC PHA-L	22.8	17.7	Lung fibroblast IL-4	28.5	29.1
Ramos (B cell) none	24.1	19.3	Lung fibroblast IL-9	23.0	23.3
Ramos (B cell) ionomycin	100.0	100.0	Lung fibroblast IL-13	20.6	18.9
B lymphocytes PWM	71.7	74.2	Lung fibroblast IFN gamma	39.0	32.5
B lymphocytes CD40L and IL-4	29.1	28.7	Dermal fibroblast CCD1070 rest	33.9	31.0
EOL-1 dbcAMP	12.1	10.5	Dermal fibroblast CCD1070 TNF alpha	76.8	62.0
EOL-1 dbcAMP PMA/ionomycin	14.5	10.9	Dermal fibroblast CCD1070 IL-1 beta	20.3	13.9
Dendritic cells none	13.2	14.8	Dermal fibroblast IFN gamma	14.2	9.5
Dendritic cells LPS	11.7	8.3	Dermal fibroblast IL-4	26.4	20.4
Dendritic cells anti- CD40	17.7	12.7	IBD Colitis 2	2.6	2.2
Monocytes rest	16.7	17.6	IBD Crohn's	2.0	1.9
Monocytes LPS	6.4	5.0	Colon	11.9	10.5
Macrophages rest	23.5	22.8	Lung	13.3	11.2
Macrophages LPS	9.9	7.1	Thymus	14.4	12.9
HUVEC none	20.6	17.9	Kidney	27.5	19.6

NS neurodegeneration V1.0 Summary, 1998, 1999, 2000, 2001, 2002, 2003, 2004, 2005, 2006, 2007, 2008, 2009, 2010, 2011, 2012, 2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020, 2021, 2022, 2023, 2024, 2025, 2026, 2027, 2028, 2029, 2030, 2031, 2032, 2033, 2034, 2035, 2036, 2037, 2038, 2039, 2040, 2041, 2042, 2043, 2044, 2045, 2046, 2047, 2048, 2049, 2050, 2051, 2052, 2053, 2054, 2055, 2056, 2057, 2058, 2059, 2060, 2061, 2062, 2063, 2064, 2065, 2066, 2067, 2068, 2069, 2070, 2071, 2072, 2073, 2074, 2075, 2076, 2077, 2078, 2079, 2080, 2081, 2082, 2083, 2084, 2085, 2086, 2087, 2088, 2089, 2090, 2091, 2092, 2093, 2094, 2095, 2096, 2097, 2098, 2099, 2100, 2101, 2102, 2103, 2104, 2105, 2106, 2107, 2108, 2109, 2110, 2111, 2112, 2113, 2114, 2115, 2116, 2117, 2118, 2119, 2120, 2121, 2122, 2123, 2124, 2125, 2126, 2127, 2128, 2129, 2130, 2131, 2132, 2133, 2134, 2135, 2136, 2137, 2138, 2139, 2140, 2141, 2142, 2143, 2144, 2145, 2146, 2147, 2148, 2149, 2150, 2151, 2152, 2153, 2154, 2155, 2156, 2157, 2158, 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expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3373 Highest expression of the CG58564-01 gene is seen in a prostate cancer cell line (CT=27). Overall, this gene is expressed at moderate levels in the cancer cell lines in this panel. A higher level of expression is observed in clusters of cell lines derived from prostate, brain, melanoma, colon, lung, breast and ovarian cancer when compared to expression in normal prostate, brain, colon, lung, breast and ovary. Thus, this gene could potentially be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, this gene product has moderate levels of expression in adipose, heart, skeletal muscle, adrenal, pituitary, thyroid and pancreas. Thus, this gene product may be a small molecule target for the treatment of endocrine and metabolic diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene appears to be differentially expressed in fetal (CT value = 29) vs adult liver (CT value =33) and may be useful for differentiation between the two sources of this tissue.

This gene is also expressed at moderate levels in all central nervous system samples present on this panel. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

Panel 1.3D Summary: Ag3023 The CG58564-01 gene is ubiquitously expressed among the samples on this panel, with highest expression in an ovarian cancer cell line (CT=28.8). Overall, the expression of this gene shows good agreement with panel 1.4. A higher level of expression is observed in prostate, brain, melanoma, colon, lung, pancreatic, breast and ovarian cancer cell lines than the normal prostate, brain, colon, lung, pancreas, breast and ovary. Thus, expression of this gene could be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Ag3023 The CG58564-01 gene is ubiquitously expressed among the samples on this panel. Please see Panel 1.4 for discussion of utility of this gene in metabolic disease.

This gene represents a phosphatase that is also expressed at low to moderate levels across the CNS. Some phosphatases comprise a family of MAP kinase regulating enzymes, members of which are upregulated in brains subjected to insults such as ischemia and seizure activity. MAP kinases are known to regulate neurotrophic and neurotoxic pathways. Consequently, agents that modulate the activity of this gene may have utility in attenuating the apoptotic and neurodegenerative processes following brain insults.

References:

1. Wiessner C. The dual specificity phosphatase PAC-1 is transcriptionally induced in the rat brain following transient forebrain ischemia. *Brain Res Mol Brain Res* 1995 Feb;28(2):353-6
2. Boschert U, Muda M, Camps M, Dickinson R, Arkininstall S. Induction of the dual specificity phosphatase PAC1 in rat brain following seizure activity. *Neuroreport* 1997 Sep 29;8(14):3077-80

Panel 4D Summary: Ag3023/Ag3373 The CG585864-01 gene is expressed at high to moderate levels in a wide range of cell types and tissues of significance in the immune response in health and disease. Highest expression of this gene is seen in ionomycin treated Ramos B cells (CT=26.83). Therefore, targeting of this gene product with a small molecule drug or antibody therapeutic may modulate the functions of cells of the immune system as well as resident tissue cells and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, and arthritis, including osteoarthritis and rheumatoid arthritis.

M. CG58564-03: Dual specificity phosphatase

Expression of gene CG58564-03 was assessed using the primer-probe sets Ag3023, Ag3373 and Ag5847, described in Tables MA, MB and MC. Results of the RTQ-PCR runs are shown in Tables MD, ME, MF, MG and MH.

Table MA. Probe Name Ag3023

Primer	Sequence	Start	End	Position	Size
Forward	tttaatgttggaattgttcaatca	22	261	408	

Probe	TET-5' - tcaggaatatgaagccatctacctagca - 3' - TAMRA	28	230	409
Reverse	5' - tggagtgggtgacatcatctgta - 3'	22	198	410

Table MB. Probe Name Ag3373

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - atttgccatcaacttcaggaa - 3'	22	251	411
Probe	TET-5' - tgaagccatctacctagcaaaattaaca - 3' - TAMRA	28	221	412
Reverse	5' - tggagtgggtgacatcatctgta - 3'	22	198	413

Table MC. Probe Name Ag5847

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - cattccaaatgtttctgtagt - 3'	21	335	414
Probe	TET-5' - ttcatagcagatgaatatgggcctaagaac - 3' - TAMRA	30	371	415
Reverse	5' - ccacagtgaaggaagac - 3'	18	457	416

Table MD. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071	Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071
AD 1 Hippo	10.9	16.8	Control (Path) 3 Temporal Ctx	9.1	8.0
AD 2 Hippo	34.2	37.6	Control (Path) 4 Temporal Ctx	40.6	65.5
AD 3 Hippo	12.0	15.8	AD 1 Occipital Ctx	24.7	29.1
AD 4 Hippo	13.8	10.3	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 6 Hippo	80.7	72.2	AD 4	35.4	22.4

			Occipital Ctx		
Control 2 Hippo	35.8	38.4	AD 5 Occipital Ctx	3.9	30.4
Control 4 Hippo	16.5	11.7	AD 6 Occipital Ctx	46.0	37.4
Control (Path) 3 Hippo	13.1	15.4	Control 1 Occipital Ctx	9.9	10.7
AD 1 Temporal Ctx	39.0	31.4	Control 2 Occipital Ctx	39.0	38.4
AD 2 Temporal Ctx	38.7	73.2	Control 3 Occipital Ctx	23.0	20.6
AD 3 Temporal Ctx	9.5	13.2	Control 4 Occipital Ctx	13.3	13.3
AD 4 Temporal Ctx	27.9	34.9	Control (Path) 1 Occipital Ctx	80.1	76.3
AD 5 Inf Temporal Ctx	59.0	100.0	Control (Path) 2 Occipital Ctx	17.3	20.0
AD 5 SupTemporal Ctx	33.2	44.1	Control (Path) 3 Occipital Ctx	8.4	8.7
AD 6 Inf Temporal Ctx	100.0	73.2	Control (Path) 4 Occipital Ctx	21.2	20.6
AD 6 Sup Temporal Ctx	79.6	80.1	Control 1 Parietal Ctx	12.1	16.3
Control 1 Temporal Ctx	10.2	13.7	Control 2 Parietal Ctx	48.0	40.9
Control 2 Temporal Ctx	41.2	31.9	Control 3 Parietal Ctx	17.9	16.3
			Control		
Control 4 Temporal Ctx	9.5	9.5	Control (Path) 2	28.9	29.9

			Parietal Ctx		
Control (Path) 1 Temporal Ctx	59.9	68.3	Control (Path) 3 Parietal Ctx	10.2	9.0
Control (Path) 2 Temporal Ctx	40.3	41.2	Control (Path) 4 Parietal Ctx	44.8	43.8

Table ME. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119	Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119
Adipose	12.0	Renal ca. TK-10	20.3
Melanoma* Hs688(A).T	30.8	Bladder	23.2
Melanoma* Hs688(B).T	69.3	Gastric ca. (liver met.) NCI-N87	25.3
Melanoma* M14	15.0	Gastric ca. KATO III	30.8
Melanoma* LOXIMVI	26.6	Colon ca. SW-948	9.7
Melanoma* SK- MEL-5	21.5	Colon ca. SW480	35.1
Squamous cell carcinoma SCC-4	33.0	Colon ca.* (SW480 met) SW620	13.9
Testis Pool	19.8	Colon ca. HT29	8.5
Prostate ca.* (bone met) PC-3	100.0	Colon ca. HCT-116	36.9
Prostate Pool	9.2	Colon ca. CaCo-2	42.9
Placenta	3.8	Colon cancer tissue	9.0
Uterus Pool	7.4	Colon ca. SW1116	5.8
Ovarian ca. OVCAR-3	28.5	Colon ca. Colo-205	4.3
Ovarian ca. SK-OV- 3	40.3	Colon ca. SW-48	4.2
Ovarian ca. OVCAR-4	20.0	Colon Pool	20.7
Ovarian ca. OVCAR-5	35.1	Small Intestine Pool	12.2
Ovarian ca. IGROV- 1	10.9	Stomach Pool	9.9
Ovarian ca.			
Breast ca. MCF-	87.6	Heart Pool	10.6
Breast ca. MDA-	37.1	Lymph Node Pool	17.9

MB-231			
Breast ca. BT 549	62.4	Fetal Skeletal Muscle	12.3
Breast ca. T47D	61.1	Skeletal Muscle Pool	16.0
Breast ca. MDA-N	10.0	Spleen Pool	11.6
Breast Pool	17.3	Thymus Pool	12.2
Trachea	12.0	CNS cancer (glio/astro) U87-MG	29.1
Lung	6.7	CNS cancer (glio/astro) U-118-MG	69.3
Fetal Lung	34.2	CNS cancer (neuro;met) SK-N-AS	34.9
Lung ca. NCI-N417	5.4	CNS cancer (astro) SF- 539	19.1
Lung ca. LX-1	17.2	CNS cancer (astro) SNB-75	35.8
Lung ca. NCI-H146	3.0	CNS cancer (glio) SNB-19	11.3
Lung ca. SHP-77	18.6	CNS cancer (glio) SF- 295	26.4
Lung ca. A549	29.1	Brain (Amygdala) Pool	4.5
Lung ca. NCI-H526	4.6	Brain (cerebellum)	8.1
Lung ca. NCI-H23	31.6	Brain (fetal)	13.2
Lung ca. NCI-H460	18.2	Brain (Hippocampus) Pool	5.3
Lung ca. HOP-62	14.1	Cerebral Cortex Pool	5.4
Lung ca. NCI-H522	31.6	Brain (Substantia nigra) Pool	4.8
Liver	1.2	Brain (Thalamus) Pool	8.0
Fetal Liver	32.3	Brain (whole)	6.2
Liver ca. HepG2	14.6	Spinal Cord Pool	6.6
Kidney Pool	22.1	Adrenal Gland	8.1
Fetal Kidney	26.1	Pituitary gland Pool	3.0
Renal ca. 786-0	28.7	Salivary Gland	4.7
Renal ca. A498	11.3	Thyroid (female)	4.4
Renal ca. ACHN	12.2	Pancreatic ca. CAPAN2	17.3
Renal ca. UO-31	24.1	Pancreas Pool	17.1

Table MF. General_screening_panel_v1.5

Dose 1 (0.1 mg/kg)		Dose 2 (0.5 mg/kg)	
Species	Schm. no.	Species	Schm. no.
Melanoma*	0.1	Bladder	0.1

Hs688(A).T			
Melanoma* Hs688(B).T	0.1	Gastric ca. (liver met.) NCI-N87	0.2
Melanoma* M14	0.1	Gastric ca. KATO III	0.1
Melanoma* LOXIMVI	0.1	Colon ca. SW-948	0.1
Melanoma* SK- MEL-5	0.1	Colon ca. SW480	0.2
Squamous cell carcinoma SCC-4	0.2	Colon ca.* (SW480 met) SW620	1.8
Testis Pool	0.1	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.6	Colon ca. HCT-116	0.2
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.2	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	0.1	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.1	Colon Pool	0.1
Ovarian ca. OVCAR-5	0.2	Small Intestine Pool	0.0
Ovarian ca. IGROV- 1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.1	Bone Marrow Pool	0.0
Ovary	0.1	Fetal Heart	0.1
Breast ca. MCF-7	0.3	Heart Pool	0.0
Breast ca. MDA- MB-231	0.2	Lymph Node Pool	0.1
Breast ca. BT 549	0.2	Fetal Skeletal Muscle	0.1
Breast ca. T47D	0.2	Skeletal Muscle Pool	0.1
Breast ca. MDA-N	0.1	Spleen Pool	0.1
Breast Pool	0.0	Thymus Pool	0.1
Trachea	0.1	CNS cancer (glio/astro) U87-MG	0.2
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.5

Lung ca. SW-620
CNS cancer (glio/astro)
U87-MG

Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.2
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.1
Lung ca. SHP-77	0.1	CNS cancer (glio) SF- 295	0.2
Lung ca. A549	0.2	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.1	Brain (fetal)	0.1
Lung ca. NCI-H460	0.1	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.1	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	0.0
Fetal Liver	0.1	Brain (whole)	0.0
Liver ca. HepG2	0.1	Spinal Cord Pool	0.0
Kidney Pool	0.1	Adrenal Gland	0.0
Fetal Kidney	0.1	Pituitary gland Pool	0.0
Renal ca. 786-0	0.2	Salivary Gland	100.0
Renal ca. A498	0.1	Thyroid (female)	0.0
Renal ca. ACHN	0.1	Pancreatic ca. CAPAN2	0.1
Renal ca. UO-31	0.1	Pancreas Pool	0.0

Table MG. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3023, Run 167966931	Tissue Name	Rel. Exp.(%) Ag3023, Run 167966931
Liver adenocarcinoma	51.1	Kidney (fetal)	26.2
Pancreas	6.1	Renal ca. 786-0	34.2
Pancreatic ca. CAPAN 2	17.7	Renal ca. A498	17.6
Adrenal gland	3.8	Renal ca. RXF 393	17.2
Thyroid	3.0	Renal ca. ACHN	13.5
Salivary gland	3.9	Renal ca. UO-31	0.0
Pituitary gland	3.6	Renal ca. TK-10	23.0
Brain (fetal)	8.1	Liver	11.7
Brain (whole)	8.5	Liver (fetal)	8.0
Brain (amygdala)	6.7	Liver ca.	26.2
Brain (hippocampus)	9.0	Lung (fetal)	12.9
Brain (substantia nigra)	9.0	Lung ca. (small cell)	12.9

		LX-1	
Brain (thalamus)	4.2	Lung ca. (small cell) NCI-H69	9.9
Cerebral Cortex	2.0	Lung ca. (s.cell var.) SHP-77	67.8
Spinal cord	6.9	Lung ca. (large cell)NCI-H460	3.4
Glio/astro U87-MG	28.5	Lung ca. (non-sm. cell) A549	45.1
Glio/astro U-118-MG	46.7	Lung ca. (non-s.cell) NCI-H23	22.7
astrocytoma SW1783	40.6	Lung ca. (non-s.cell) HOP-62	25.7
neuro*; met SK-N-AS	27.2	Lung ca. (non-s.cl) NCI-H522	38.2
astrocytoma SF-539	29.7	Lung ca. (squam.) SW 900	27.4
astrocytoma SNB-75	35.1	Lung ca. (squam.) NCI-H596	29.9
glioma SNB-19	15.6	Mammary gland	5.1
glioma U251	37.9	Breast ca.* (pl.ef) MCF-7	47.0
glioma SF-295	18.4	Breast ca.* (pl.ef) MDA-MB-231	22.7
Heart (fetal)	2.9	Breast ca.* (pl.ef) T47D	86.5
Heart	12.9	Breast ca. BT-549	15.9
Skeletal muscle (fetal)	3.4	Breast ca. MDA-N	10.4
Skeletal muscle	36.3	Ovary	2.9
Bone marrow	4.5	Ovarian ca. OVCAR- 3	26.1
Thymus	14.3	Ovarian ca. OVCAR- 4	16.3
Spleen	8.7	Ovarian ca. OVCAR- 5	83.5
Lymph node	11.8	Ovarian ca. OVCAR- 8	9.3
Colorectal	10.4	Ovarian ca. IGROV- 1	12.0
Stomach	7.8	Ovarian ca.* (ascites) SK-OV-3	100.0
Colon ca.* SW620(SW480 met)	42.9	Prostate	2.9

Colon ca. HT29	9.9	Prostate ca.* (bone met)PC-3	78.5
Colon ca. HCT-116	26.2	Testis	9.7
Colon ca. CaCo-2	41.5	Melanoma Hs688(A).T	5.9
Colon ca. tissue(ODO3866)	6.3	Melanoma* (met) Hs688(B).T	14.2
Colon ca. HCC-2998	16.0	Melanoma UACC-62	14.0
Gastric ca.* (liver met) NCI-N87	18.8	Melanoma M14	5.7
Bladder	30.6	Melanoma LOX IMVI	8.8
Trachea	3.2	Melanoma* (met) SK-MEL-5	14.7
Kidney	9.6	Adipose	18.9

Table MH. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3023, Run 164516146	Rel. Exp.(%) Ag3373, Run 165296617	Tissue Name	Rel. Exp.(%) Ag3023, Run 164516146	Rel. Exp.(%) Ag3373, Run 165296617
Secondary Th1 act	18.6	17.9	HUVEC IL-1beta	20.3	18.6
Secondary Th2 act	24.3	28.5	HUVEC IFN gamma	25.3	22.7
Secondary Tr1 act	22.8	21.8	HUVEC TNF alpha + IFN gamma	16.3	18.0
Secondary Th1 rest	7.5	6.8	HUVEC TNF alpha + IL4	18.2	13.4
Secondary Th2 rest	11.6	9.5	HUVEC IL-11	13.7	9.9
Secondary Tr1 rest	12.1	10.7	Lung Microvascular EC none	25.7	21.6
Primary Th1 act	20.7	16.5	Lung Microvascular EC TNFalpha + IL-1beta	26.2	18.3
Primary Th2 act	20.2	19.3	Microvascular Dermal EC none	27.5	21.3

Primary Th1 rest	51.1	51.4	IL1beta Bronchial	13.0	16.3
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			epithelium TNFalpha + IL1beta		
Primary Th2 rest	26.2	29.5	Small airway epithelium none	8.1	8.5
Primary Tr1 rest	23.7	26.1	Small airway epithelium TNFalpha + IL- 1beta	50.3	39.8
CD45RA CD4 lymphocyte act	14.6	11.0	Coronary artery SMC rest	20.2	18.9
CD45RO CD4 lymphocyte act	25.2	22.4	Coronary artery SMC TNFalpha + IL-1beta	12.0	9.8
CD8 lymphocyte act	20.4	15.8	Astrocytes rest	10.4	11.1
Secondary CD8 lymphocyte rest	16.5	19.9	Astrocytes TNFalpha + IL- 1beta	11.7	9.8
Secondary CD8 lymphocyte act	13.2	9.3	KU-812 (Basophil) rest	47.6	38.2
CD4 lymphocyte none	17.1	11.6	KU-812 (Basophil) PMA/ionomycin	94.0	92.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	18.3	16.6	CCD1106 (Keratinocytes) none	19.9	13.2
LAK cells rest	25.5	16.0	CCD1106 (Keratinocytes) TNFalpha + IL- 1beta	6.0	4.8
LAK cells IL-2	27.2	22.5	Liver cirrhosis	3.1	2.7
LAK cells IL-2+IL- 12	27.2	19.3	Lupus kidney	2.1	1.7
LAK cells IL- 2+IFN gamma	36.3	34.4	NCI-H292 none	30.1	18.9
LAK cells IL-2+ IL-18	35.1	29.7	NCI-H292 IL-4	33.9	34.6
LAK cells PMA/ionomycin	12.4	11.0	NCI-H292 IL-9	40.1	29.1
NK Cells IL-2 rest	20.0	15.0	NCI-H292 IL-13	16.2	14.2
Two Way MLR 3	21.0	16.7	NCI-H292 IFN	16.6	18.4
Two Way MLR 7	11.4	9.5	HPAEC TNF	25.3	25.3

day			alpha + IL-1 beta		
PBMC rest	13.7	10.5	Lung fibroblast none	11.4	14.2
PBMC PWM	69.3	66.4	Lung fibroblast TNF alpha + IL-1 beta	6.1	7.2
PBMC PHA-L	22.8	17.7	Lung fibroblast IL-4	28.5	29.1
Ramos (B cell) none	24.1	19.3	Lung fibroblast IL-9	23.0	23.3
Ramos (B cell) ionomycin	100.0	100.0	Lung fibroblast IL-13	20.6	18.9
B lymphocytes PWM	71.7	74.2	Lung fibroblast IFN gamma	39.0	32.5
B lymphocytes CD40L and IL-4	29.1	28.7	Dermal fibroblast CCD1070 rest	33.9	31.0
EOL-1 dbcAMP	12.1	10.5	Dermal fibroblast CCD1070 TNF alpha	76.8	62.0
EOL-1 dbcAMP PMA/ionomycin	14.5	10.9	Dermal fibroblast CCD1070 IL-1 beta	20.3	13.9
Dendritic cells none	13.2	14.8	Dermal fibroblast IFN gamma	14.2	9.5
Dendritic cells LPS	11.7	8.3	Dermal fibroblast IL-4	26.4	20.4
Dendritic cells anti- CD40	17.7	12.7	IBD Colitis 2	2.6	2.2
Monocytes rest	16.7	17.6	IBD Crohn's	2.0	1.9
Monocytes LPS	6.4	5.0	Colon	11.9	10.5
Macrophages rest	23.5	22.8	Lung	13.3	11.2
Macrophages LPS	9.9	7.1	Thymus	14.4	12.9
HUVEC none	20.6	17.9	Kidney	27.5	19.6
HUVEC starved	43.5	38.4			

CNS_neurodegeneration_v1.0 Summary: Ag3023/Ag3373 This panel does not show differential expression of the CG56804-03 gene, a splice variant of CG56804-01, in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

AG3023 (PBMC) and Ag3373 (colon) only the splice variant CG56804-03. Expression of this

General_screening_panel_v1.4 Summary: Ag3373 Highest expression of the CG56804-03 gene is seen in a prostate cancer cell line (CT=27). Overall, this gene is expressed at moderate levels in the cancer cell lines in this panel. A higher level of expression is observed in clusters of cell lines derived from prostate, brain, melanoma, colon, lung, breast and ovarian cancer when compared to expression in normal prostate, brain, colon, lung, breast and ovary. Thus, this gene could potentially be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, this gene product has moderate levels of expression in adipose, heart, skeletal muscle, adrenal, pituitary, thyroid and pancreas. Thus, this gene product may be a small molecule target for the treatment of endocrine and metabolic diseases, including obesity and Types 1 and 2 diabetes

In addition, this gene appears to be differentially expressed in fetal (CT value = 29) vs adult liver (CT value =33) and may be useful for differentiation between the two sources of this tissue.

This gene is also expressed at moderate levels in all central nervous system samples present on this panel. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

General_screening_panel_v1.5 Summary: Ag5847 - This primer pair, specific to this splice variant, CG58564-03. Expression of this variant is highest in salivary gland (CT=28.6). Therefore, expression of this gene can be used to differentiate this sample from others on the panel.

Panel 1.3D Summary: Ag3023 The CG56804-03 gene is ubiquitously expressed among the samples on this panel, with highest expression in an ovarian cancer cell line (CT=28.8). Overall, the expression of this gene shows good agreement with panel 1.4. A higher level of expression is observed in prostate, brain, melanoma, colon, lung, pancreatic, breast and ovarian cancer cell lines than the normal prostate, brain, colon, lung, pancreas, breast and

ovarian cancer cell lines than the normal prostate, brain, colon, lung, pancreas, breast and

may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, expression of this gene is widespread, as in the previous panel. Please see Panel 1.4 for discussion of utility of this gene in metabolic disease.

This gene represents a dual specificity phosphatase that is also expressed at low to moderate levels across the CNS. Dual-specificity phosphatases comprise a family of MAP kinase regulating enzymes, members of which are upregulated in brains subjected to insults such as ischemia and seizure activity. MAP kinases are known to regulate neurotrophic and neurotoxic pathways. Consequently, agents that modulate the activity of this gene may have utility in attenuating the apoptotic and neurodegenerative processes following brain insults.

Panel 4.1D Summary: Ag5847 - This primer pair recognizes a splice variant of CG58564-03. Expression of this variant is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3023/Ag3373 The CG56804-03 gene is expressed at high to moderate levels in a wide range of cell types and tissues of significance in the immune response in health and disease. Highest expression of this gene is seen in ionomycin treated Ramos B cells (CT=26.83). Therefore, targeting of this gene product with a small molecule drug or antibody therapeutic may modulate the functions of cells of the immune system as well as resident tissue cells and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, and arthritis, including osteoarthritis and rheumatoid arthritis.

N. CG58564-04: Dual specificity phosphatase

Expression of gene CG58564-04, a splice variant of CG58564-01, was assessed using the primer-probe sets Ag3023, Ag3373 and Ag5844, described in Tables NA, NB and NC. Results of the RTQ-PCR runs are shown in Tables ND, NE, NF and NG.

Table NA. Probe Name Ag3023

Primers	Sequences	Length	Position	NO:
Forward	5'-ctaagtctggatttgccatca-3'	22	190	417

Probe	TET-5' - tcaggaatatgaagccatctacctagca - 3' - TAMRA	28	159	418
Reverse	5' - tggagtgggtgacatcatctgta - 3'	22	127	419

Table NB. Probe Name Ag3373

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - atttgtccatcaacttcaggaa - 3'	22	180	420
Probe	TET-5' - tgaagccatctacctagcaaaattaaca - 3' - TAMRA	28	150	421
Reverse	5' - tggagtgggtgacatcatctgta - 3'	22	127	422

Table NC. Probe Name Ag5844

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - ccttagtctaaataactgctg - 3'	21	377	423
Probe	TET-5' - agtttgcttcaatatatttgctgatgcata - 3' - TAMRA	30	415	424
Reverse	5' - aggagtggacctaccctat - 3'	19	552	425

Table ND. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071	Tissue Name	Rel. Exp.(%) Ag3023, Run 209821074	Rel. Exp.(%) Ag3373, Run 210154071
AD 1 Hippo	10.9	16.8	Control (Path) 3 Temporal Ctx	9.1	8.0
AD 2 Hippo	34.2	37.6	Control (Path) 4 Temporal Ctx	40.6	65.5
AD 3 Hippo	12.0	15.8	AD 1 Occipital Ctx	24.7	29.1
AD 4 Hippo	13.8	10.3	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 6 Hippo	80.7	72.2	AD 4	35.4	22.4

			Occipital Ctx		
Control 2 Hippo	35.8	38.4	AD 5 Occipital Ctx	3.9	30.4
Control 4 Hippo	16.5	11.7	AD 6 Occipital Ctx	46.0	37.4
Control (Path) 3 Hippo	13.1	15.4	Control 1 Occipital Ctx	9.9	10.7
AD 1 Temporal Ctx	39.0	31.4	Control 2 Occipital Ctx	39.0	38.4
AD 2 Temporal Ctx	38.7	73.2	Control 3 Occipital Ctx	23.0	20.6
AD 3 Temporal Ctx	9.5	13.2	Control 4 Occipital Ctx	13.3	13.3
AD 4 Temporal Ctx	27.9	34.9	Control (Path) 1 Occipital Ctx	80.1	76.3
AD 5 Inf Temporal Ctx	59.0	100.0	Control (Path) 2 Occipital Ctx	17.3	20.0
AD 5 Sup Temporal Ctx	33.2	44.1	Control (Path) 3 Occipital Ctx	8.4	8.7
AD 6 Inf Temporal Ctx	100.0	73.2	Control (Path) 4 Occipital Ctx	21.2	20.6
AD 6 Sup Temporal Ctx	79.6	80.1	Control 1 Parietal Ctx	12.1	16.3
Control 1 Temporal Ctx	10.2	13.7	Control 2 Parietal Ctx	48.0	40.9
Control 2 Temporal Ctx	41.2	31.9	Control 3 Parietal Ctx	17.9	16.3
			Control		
Control 4 Temporal Ctx	9.5	9.9	Control (Path) 2	23.0	20.6

			Parietal Ctx		
Control (Path) 1 Temporal Ctx	59.9	68.3	Control (Path) 3 Parietal Ctx	10.2	9.0
Control (Path) 2 Temporal Ctx	40.3	41.2	Control (Path) 4 Parietal Ctx	44.8	43.8

Table NE. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119	Tissue Name	Rel. Exp.(%) Ag3373, Run 217043119
Adipose	12.0	Renal ca. TK-10	20.3
Melanoma* Hs688(A).T	30.8	Bladder	23.2
Melanoma* Hs688(B).T	69.3	Gastric ca. (liver met.) NCI-N87	25.3
Melanoma* M14	15.0	Gastric ca. KATO III	30.8
Melanoma* LOXIMVI	26.6	Colon ca. SW-948	9.7
Melanoma* SK- MEL-5	21.5	Colon ca. SW480	35.1
Squamous cell carcinoma SCC-4	33.0	Colon ca.* (SW480 met) SW620	13.9
Testis Pool	19.8	Colon ca. HT29	8.5
Prostate ca.* (bone met) PC-3	100.0	Colon ca. HCT-116	36.9
Prostate Pool	9.2	Colon ca. CaCo-2	42.9
Placenta	3.8	Colon cancer tissue	9.0
Uterus Pool	7.4	Colon ca. SW1116	5.8
Ovarian ca. OVCAR-3	28.5	Colon ca. Colo-205	4.3
Ovarian ca. SK-OV- 3	40.3	Colon ca. SW-48	4.2
Ovarian ca. OVCAR-4	20.0	Colon Pool	20.7
Ovarian ca. OVCAR-5	35.1	Small Intestine Pool	12.2
Ovarian ca. IGROV- 1	10.9	Stomach Pool	9.9
Ovarian ca. SK-OV-3			
Breast ca. MCF	37.6	Heart Pool	10.6
Breast ca. MDA-	37.1	Lymph Node Pool	17.9

MB-231			
Breast ca. BT 549	62.4	Fetal Skeletal Muscle	12.3
Breast ca. T47D	61.1	Skeletal Muscle Pool	16.0
Breast ca. MDA-N	10.0	Spleen Pool	11.6
Breast Pool	17.3	Thymus Pool	12.2
Trachea	12.0	CNS cancer (glio/astro) U87-MG	29.1
Lung	6.7	CNS cancer (glio/astro) U-118-MG	69.3
Fetal Lung	34.2	CNS cancer (neuro;met) SK-N-AS	34.9
Lung ca. NCI-N417	5.4	CNS cancer (astro) SF- 539	19.1
Lung ca. LX-1	17.2	CNS cancer (astro) SNB-75	35.8
Lung ca. NCI-H146	3.0	CNS cancer (glio) SNB-19	11.3
Lung ca. SHP-77	18.6	CNS cancer (glio) SF- 295	26.4
Lung ca. A549	29.1	Brain (Amygdala) Pool	4.5
Lung ca. NCI-H526	4.6	Brain (cerebellum)	8.1
Lung ca. NCI-H23	31.6	Brain (fetal)	13.2
Lung ca. NCI-H460	18.2	Brain (Hippocampus) Pool	5.3
Lung ca. HOP-62	14.1	Cerebral Cortex Pool	5.4
Lung ca. NCI-H522	31.6	Brain (Substantia nigra) Pool	4.8
Liver	1.2	Brain (Thalamus) Pool	8.0
Fetal Liver	32.3	Brain (whole)	6.2
Liver ca. HepG2	14.6	Spinal Cord Pool	6.6
Kidney Pool	22.1	Adrenal Gland	8.1
Fetal Kidney	26.1	Pituitary gland Pool	3.0
Renal ca. 786-0	28.7	Salivary Gland	4.7
Renal ca. A498	11.3	Thyroid (female)	4.4
Renal ca. ACHN	12.2	Pancreatic ca. CAPAN2	17.3
Renal ca. UO-31	24.1	Pancreas Pool	17.1

Table NF. Panel 1.3D

	Ref. Exp. (9) A-3023	Ref. Exp. (9) A-3023
Pancreas	6.1	Renal ca. 786-0
		34.2

Pancreatic ca. CAPAN 2	17.7	Renal ca. A498	17.6
Adrenal gland	3.8	Renal ca. RXF 393	17.2
Thyroid	3.0	Renal ca. ACHN	13.5
Salivary gland	3.9	Renal ca. UO-31	0.0
Pituitary gland	3.6	Renal ca. TK-10	23.0
Brain (fetal)	8.1	Liver	11.7
Brain (whole)	8.5	Liver (fetal)	8.0
Brain (amygdala)	6.7	Liver ca. (hepatoblast) HepG2	26.2
Brain (cerebellum)	15.2	Lung	3.1
Brain (hippocampus)	5.4	Lung (fetal)	11.0
Brain (substantia nigra)	9.0	Lung ca. (small cell) LX-1	12.9
Brain (thalamus)	4.2	Lung ca. (small cell) NCI-H69	9.9
Cerebral Cortex	2.0	Lung ca. (s.cell var.) SHP-77	67.8
Spinal cord	6.9	Lung ca. (large cell) NCI-H460	3.4
Glio/astro U87-MG	28.5	Lung ca. (non-sm. cell) A549	45.1
Glio/astro U-118-MG	46.7	Lung ca. (non-s.cell) NCI-H23	22.7
astrocytoma SW1783	40.6	Lung ca. (non-s.cell) HOP-62	25.7
neuro*; met SK-N-AS	27.2	Lung ca. (non-s.cl) NCI-H522	38.2
astrocytoma SF-539	29.7	Lung ca. (squam.) SW 900	27.4
astrocytoma SNB-75	35.1	Lung ca. (squam.) NCI-H596	29.9
glioma SNB-19	15.6	Mammary gland	5.1
glioma U251	37.9	Breast ca.* (pl.ef) MCF-7	47.0
glioma SF-295	18.4	Breast ca.* (pl.ef) MDA-MB-231	22.7
Heart (fetal)	2.9	Breast ca.* (pl.ef) T47D	86.5
Heart	12.9	Breast ca. BT-549	15.9
Bone marrow	1.5	Breast ca. BT-20	1.1
		Breast ca. SK-BR-3	1.1
		Breast ca. ZR-75.1	1.1
		Breast ca. ZR-73.1	1.1
		Breast ca. ZR-75.2	1.1
		Breast ca. ZR-75.3	1.1
		Breast ca. ZR-75.4	1.1
		Breast ca. ZR-75.5	1.1
		Breast ca. ZR-75.6	1.1
		Breast ca. ZR-75.7	1.1
		Breast ca. ZR-75.8	1.1
		Breast ca. ZR-75.9	1.1
		Breast ca. ZR-75.10	1.1
		Breast ca. ZR-75.11	1.1
		Breast ca. ZR-75.12	1.1
		Breast ca. ZR-75.13	1.1
		Breast ca. ZR-75.14	1.1
		Breast ca. ZR-75.15	1.1
		Breast ca. ZR-75.16	1.1
		Breast ca. ZR-75.17	1.1
		Breast ca. ZR-75.18	1.1
		Breast ca. ZR-75.19	1.1
		Breast ca. ZR-75.20	1.1
		Breast ca. ZR-75.21	1.1
		Breast ca. ZR-75.22	1.1
		Breast ca. ZR-75.23	1.1
		Breast ca. ZR-75.24	1.1
		Breast ca. ZR-75.25	1.1
		Breast ca. ZR-75.26	1.1
		Breast ca. ZR-75.27	1.1
		Breast ca. ZR-75.28	1.1
		Breast ca. ZR-75.29	1.1
		Breast ca. ZR-75.30	1.1
		Breast ca. ZR-75.31	1.1
		Breast ca. ZR-75.32	1.1
		Breast ca. ZR-75.33	1.1
		Breast ca. ZR-75.34	1.1
		Breast ca. ZR-75.35	1.1
		Breast ca. ZR-75.36	1.1
		Breast ca. ZR-75.37	1.1
		Breast ca. ZR-75.38	1.1
		Breast ca. ZR-75.39	1.1
		Breast ca. ZR-75.40	1.1
		Breast ca. ZR-75.41	1.1
		Breast ca. ZR-75.42	1.1
		Breast ca. ZR-75.43	1.1
		Breast ca. ZR-75.44	1.1
		Breast ca. ZR-75.45	1.1
		Breast ca. ZR-75.46	1.1
		Breast ca. ZR-75.47	1.1
		Breast ca. ZR-75.48	1.1
		Breast ca. ZR-75.49	1.1
		Breast ca. ZR-75.50	1.1
		Breast ca. ZR-75.51	1.1
		Breast ca. ZR-75.52	1.1
		Breast ca. ZR-75.53	1.1
		Breast ca. ZR-75.54	1.1
		Breast ca. ZR-75.55	1.1
		Breast ca. ZR-75.56	1.1
		Breast ca. ZR-75.57	1.1
		Breast ca. ZR-75.58	1.1
		Breast ca. ZR-75.59	1.1
		Breast ca. ZR-75.60	1.1
		Breast ca. ZR-75.61	1.1
		Breast ca. ZR-75.62	1.1
		Breast ca. ZR-75.63	1.1
		Breast ca. ZR-75.64	1.1
		Breast ca. ZR-75.65	1.1
		Breast ca. ZR-75.66	1.1
		Breast ca. ZR-75.67	1.1
		Breast ca. ZR-75.68	1.1
		Breast ca. ZR-75.69	1.1
		Breast ca. ZR-75.70	1.1
		Breast ca. ZR-75.71	1.1
		Breast ca. ZR-75.72	1.1
		Breast ca. ZR-75.73	1.1
		Breast ca. ZR-75.74	1.1
		Breast ca. ZR-75.75	1.1
		Breast ca. ZR-75.76	1.1
		Breast ca. ZR-75.77	1.1
		Breast ca. ZR-75.78	1.1
		Breast ca. ZR-75.79	1.1
		Breast ca. ZR-75.80	1.1
		Breast ca. ZR-75.81	1.1
		Breast ca. ZR-75.82	1.1
		Breast ca. ZR-75.83	1.1
		Breast ca. ZR-75.84	1.1
		Breast ca. ZR-75.85	1.1
		Breast ca. ZR-75.86	1.1
		Breast ca. ZR-75.87	1.1
		Breast ca. ZR-75.88	1.1
		Breast ca. ZR-75.89	1.1
		Breast ca. ZR-75.90	1.1
		Breast ca. ZR-75.91	1.1
		Breast ca. ZR-75.92	1.1
		Breast ca. ZR-75.93	1.1
		Breast ca. ZR-75.94	1.1
		Breast ca. ZR-75.95	1.1
		Breast ca. ZR-75.96	1.1
		Breast ca. ZR-75.97	1.1
		Breast ca. ZR-75.98	1.1
		Breast ca. ZR-75.99	1.1
		Breast ca. ZR-75.100	1.1

Thymus	14.3	Ovarian ca. OVCAR-4	16.3
Spleen	8.7	Ovarian ca. OVCAR-5	83.5
Lymph node	11.8	Ovarian ca. OVCAR-8	9.3
Colorectal	10.4	Ovarian ca. IGROV-1	12.0
Stomach	7.8	Ovarian ca.* (ascites) SK-OV-3	100.0
Small intestine	5.1	Uterus	4.9
Colon ca. SW480	19.3	Placenta	1.3
Colon ca.* SW620(SW480 met)	42.9	Prostate	3.9
Colon ca. HT29	9.9	Prostate ca.* (bone met)PC-3	78.5
Colon ca. HCT-116	26.2	Testis	9.7
Colon ca. CaCo-2	41.5	Melanoma Hs688(A).T	5.9
Colon ca. tissue(ODO3866)	6.3	Melanoma* (met) Hs688(B).T	14.2
Colon ca. HCC-2998	16.0	Melanoma UACC-62	14.0
Gastric ca.* (liver met) NCI-N87	18.8	Melanoma M14	5.7
Bladder	30.6	Melanoma LOX IMVI	8.8
Trachea	3.2	Melanoma* (met) SK-MEL-5	14.7
Kidney	9.6	Adipose	18.9

Table NG. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3023, Run 164516146	Rel. Exp.(%) Ag3373, Run 165296617	Tissue Name	Rel. Exp.(%) Ag3023, Run 164516146	Rel. Exp.(%) Ag3373, Run 165296617
Secondary Th1 act	18.6	17.9	HUVEC IL-1beta	20.3	18.6
Secondary Th2 act	24.3	28.5	HUVEC IFN gamma	25.3	22.7
			HUVEC TNF		
Secondary Th1 rest	2	0.8	HUVEC TNF alpha + IL4	1.2	0.8

Secondary Th2 rest	11.6	9.5	HUVEC IL-11	13.7	9.9
Secondary Tr1 rest	12.1	10.7	Lung Microvascular EC none	25.7	21.6
Primary Th1 act	20.7	16.5	Lung Microvascular EC TNFalpha + IL- 1beta	26.2	18.3
Primary Th2 act	20.2	19.3	Microvascular Dermal EC none	27.5	21.3
Primary Tr1 act	23.3	27.7	Microvascular Dermal EC TNFalpha + IL- 1beta	20.7	19.9
Primary Th1 rest	51.1	51.4	Bronchial epithelium TNFalpha + IL1beta	13.0	16.3
Primary Th2 rest	26.2	29.5	Small airway epithelium none	8.1	8.5
Primary Tr1 rest	23.7	26.1	Small airway epithelium TNFalpha + IL- 1beta	50.3	39.8
CD45RA CD4 lymphocyte act	14.6	11.0	Coronary artery SMC rest	20.2	18.9
CD45RO CD4 lymphocyte act	25.2	22.4	Coronary artery SMC TNFalpha + IL-1beta	12.0	9.8
CD8 lymphocyte act	20.4	15.8	Astrocytes rest	10.4	11.1
Secondary CD8 lymphocyte rest	16.5	19.9	Astrocytes TNFalpha + IL- 1beta	11.7	9.8
Secondary CD8 lymphocyte act	13.2	9.3	KU-812 (Basophil) rest	47.6	38.2
CD4 lymphocyte none	17.1	11.6	KU-812 (Basophil) PMA/ionomycin	94.0	92.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	18.3	16.6	CCD1106 (Keratinocytes) none	19.9	13.2
			CCD1106		
			beta		
LAK cells IL-2	27.2	22.5	Liver cirrhosis	3.1	2.7

LAK cells IL-2+IL-12	27.2	19.3	Lupus kidney	2.1	1.7
LAK cells IL-2+IFN gamma	36.3	34.4	NCI-H292 none	30.1	18.9
LAK cells IL-2+IL-18	35.1	29.7	NCI-H292 IL-4	33.9	34.6
LAK cells PMA/ionomycin	12.4	11.0	NCI-H292 IL-9	40.1	29.1
NK Cells IL-2 rest	20.0	15.0	NCI-H292 IL-13	16.2	14.2
Two Way MLR 3 day	24.0	16.7	NCI-H292 IFN gamma	16.6	18.4
Two Way MLR 5 day	12.9	10.1	HPAEC none	13.6	13.5
Two Way MLR 7 day	11.4	9.5	HPAEC TNF alpha + IL-1 beta	25.3	25.3
PBMC rest	13.7	10.5	Lung fibroblast none	11.4	14.2
PBMC PWM	69.3	66.4	Lung fibroblast TNF alpha + IL-1 beta	6.1	7.2
PBMC PHA-L	22.8	17.7	Lung fibroblast IL-4	28.5	29.1
Ramos (B cell) none	24.1	19.3	Lung fibroblast IL-9	23.0	23.3
Ramos (B cell) ionomycin	100.0	100.0	Lung fibroblast IL-13	20.6	18.9
B lymphocytes PWM	71.7	74.2	Lung fibroblast IFN gamma	39.0	32.5
B lymphocytes CD40L and IL-4	29.1	28.7	Dermal fibroblast CCD1070 rest	33.9	31.0
EOL-1 dbcAMP	12.1	10.5	Dermal fibroblast CCD1070 TNF alpha	76.8	62.0
EOL-1 dbcAMP PMA/ionomycin	14.5	10.9	Dermal fibroblast CCD1070 IL-1 beta	20.3	13.9
Dendritic cells none	13.2	14.8	Dermal fibroblast IFN gamma	14.2	9.5
Dendritic cells LPS	11.7	8.3	Dermal fibroblast IL-4	26.4	20.4
Dendritic cells anti-CD40	17.7	12.7	IBD Colitis 2	2.6	2.2
Macrophages rest	23.5	22.8	Lung	13.5	11.2

Macrophages LPS	9.9	7.1	Thymus	14.4	12.9
HUVEC none	20.6	17.9	Kidney	27.5	19.6
HUVEC starved	43.5	38.4			

CNS_neurodegeneration_v1.0 Summary: Ag3023/Ag3373 This panel does not show differential expression of the CG56804-04 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system. Ag5847 - This primer pair recognizes a splice variant of CG58564-01 designated CG58564-04. Expression of this variant is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3373 Highest expression of the CG56804-04 gene is seen in a prostate cancer cell line (CT=27). Overall, this gene is expressed at moderate levels in the cancer cell lines in this panel. A higher level of expression is observed in clusters of cell lines derived from prostate, brain, melanoma, colon, lung, breast and ovarian cancer when compared to expression in normal prostate, brain, colon, lung, breast and ovary. Thus, this gene could potentially be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, this gene product has moderate levels of expression in adipose, heart, skeletal muscle, adrenal, pituitary, thyroid and pancreas. Thus, this gene product may be a small molecule target for the treatment of endocrine and metabolic diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene appears to be differentially expressed in fetal (CT value = 29) vs adult liver (CT value -33) and may be useful for differentiation between the two sources of this tissue.

This gene is also expressed at moderate levels in all central nervous system samples present on this panel. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

the samples on this panel (data not shown).

Panel 1.3D Summary: Ag3023 The CG56804-04 gene is ubiquitously expressed among the samples on this panel, with highest expression in an ovarian cancer cell line (CT=28.8). Overall, the expression of this gene shows good agreement with panel 1.4. A higher level of expression is observed in prostate, brain, melanoma, colon, lung, pancreatic, breast and ovarian cancer cell lines than the normal prostate, brain, colon, lung, pancreas, breast and ovary. Thus, expression of this gene could be used as a diagnostic marker of cancer in these tissues. Furthermore, inhibition of the activity of this gene product using small molecule drugs may be effective in the treatment of cancer in these tissues.

Among tissues with metabolic function, expression of this gene is widespread, as in the previous panel. Please see Panel 1.4 for discussion of utility of this gene in metabolic disease.

This gene represents a dual specificity phosphatase that is also expressed at low to moderate levels across the CNS. Dual-specificity phosphatases comprise a family of MAP kinase regulating enzymes, members of which are upregulated in brains subjected to insults such as ischemia and seizure activity. MAP kinases are known to regulate neurotrophic and neurotoxic pathways. Consequently, agents that modulate the activity of this gene may have utility in attenuating the apoptotic and neurodegenerative processes following brain insults.

Panel 4.1D Summary: Ag5844 - This primer pair recognizes a splice variant of CG58564-01. Expression of this variant is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3023/Ag3373 The CG56804-04 gene is expressed at high to moderate levels in a wide range of cell types and tissues of significance in the immune response in health and disease. Highest expression of this gene is seen in ionomycin treated Ramos B cells (CT=26.83). Therefore, targeting of this gene product with a small molecule drug or antibody therapeutic may modulate the functions of cells of the immune system as well as resident tissue cells and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, and arthritis, including osteoarthritis and rheumatoid arthritis.

CG57810-01: DPCP INTERACTING PROTEIN 1

described in Table OA. Results of the RTQ-PCR runs are shown in Tables OB and OC.

Table OA. Probe Name Ag3338

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cccattcagcactgaaacag-3'	20	3021	426
Probe	TET-5'-tcttgtaaattgacaaagaatcctctgaaca-3'- TAMRA	30	3055	427
Reverse	5'-tgcttcactgacttcagaacct-3'	22	3085	428

Table OB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3338, Run 215773746	Tissue Name	Rel. Exp.(%) Ag3338, Run 215773746
Adipose	1.1	Renal ca. TK-10	0.8
Melanoma* Hs688(A).T	0.0	Bladder	1.1
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.2	Colon ca. SW480	0.4
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	100.0	Colon ca. HT29	0.5
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.2
Prostate Pool	1.0	Colon ca. CaCo-2	1.0
Placenta	0.0	Colon cancer tissue	0.9
Uterus Pool	0.0	Colon ca. SW1116	0.2
Ovarian ca. OVCAR-3	0.9	Colon ca. Colo-205	0.2
Ovarian ca. SK-OV- 3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	1.2	Colon Pool	0.5
Ovarian ca. OVCAR-5	3.5	Small Intestine Pool	0.3
Ovarian ca. IGROV- 1	0.0	Stomach Pool	0.2

Ovary

Renal Tissue

Breast ca. MCF-7	1.9	Heart Pool	1.1
Breast ca. MDA-MB-231	1.2	Lymph Node Pool	1.4
Breast ca. BT 549	0.2	Fetal Skeletal Muscle	0.2
Breast ca. T47D	6.7	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	1.4
Breast Pool	0.5	Thymus Pool	0.0
Trachea	0.9	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.2	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.4	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.8	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.5	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.1	CNS cancer (glio) SF-295	0.2
Lung ca. A549	1.5	Brain (Amygdala) Pool	0.7
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.6
Lung ca. NCI-H23	1.5	Brain (fetal)	0.9
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.7
Lung ca. HOP-62	3.0	Cerebral Cortex Pool	0.2
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.7
Liver	0.4	Brain (Thalamus) Pool	1.3
Fetal Liver	0.5	Brain (whole)	0.0
Liver ca. HepG2	0.2	Spinal Cord Pool	0.9
Kidney Pool	0.9	Adrenal Gland	0.0
Fetal Kidney	0.6	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	3.4
Renal ca. UO-31	0.0	Pancreas Pool	0.8

Table OC Panel 4D

Tissue Name	Ag3338, Run 165221737	Tissue Name	Ag3338, Run 165221737
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Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	6.9
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	2.6
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	1.9
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	4.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	4.6	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	0.0
LAK cells IL-2+IL-12	0.0	Lupus kidney	2.4
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	4.5
LAK cells			
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0

Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	14.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	3.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	4.7	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	13.9	Dermal fibroblast IL-4	0.0
Dendritic cells anti-CD40	6.0	IBD Colitis 2	0.0
Monocytes rest	100.0	IBD Crohn's	0.0
Monocytes LPS	0.0	Colon	15.2
Macrophages rest	1.3	Lung	4.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	3.1
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3338 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3338 - Expression of this gene is highest in testis (CT=29.4). Therefore, expression of this gene could be used to distinguish this sample from others on the panel.

There is also low expression in pancreatic cancer cell line CAPAN2, lung cancer cell line HOP-62, breast cancer cell line T47D, and ovarian cancer cell line OVCAR-5. Thus,

Panel 4D Summary: Ag3338 - Significant expression of this gene is seen only in resting monocytes (CT=32.3) Therefore, expression of this gene can be used to differentiate between this sample and others on this panel.

P. CG57789-01 and CG57789-02: RAS-LIKE PROTEIN RRP22-like

Expression of gene CG57789-01 and variant CG57789-02 was assessed using the primer-probe set Ag3333, described in Table PA. Results of the RTQ-PCR runs are shown in Tables PB, PC and PD.

Table PA. Probe Name Ag3333

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tcgactttccacccatcag-3'	19	181	429
Probe	TET-5'-cttccctgtcaatacgctccaggagt-3'- TAMRA	26	203	430
Reverse	5'-aggatgtaggcgtggacact-3'	20	258	431

Table PB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3333, Run 210146459	Tissue Name	Rel. Exp.(%) Ag3333, Run 210146459
AD 1 Hippo	22.2	Control (Path) 3 Temporal Ctx	7.5
AD 2 Hippo	18.8	Control (Path) 4 Temporal Ctx	21.6
AD 3 Hippo	17.9	AD 1 Occipital Ctx	29.7
AD 4 Hippo	8.7	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	100.0	AD 3 Occipital Ctx	15.8
AD 6 Hippo	42.9	AD 4 Occipital Ctx	24.7
Control 2 Hippo	25.9	AD 5 Occipital Ctx	90.1
Control 4 Hippo	12.1	AD 6 Occipital Ctx	16.3
Control (Path) 3 Hippo	13.4	Control 1 Occipital Ctx	4.2
AD 1 Temporal Ctx	21.3	Control 2 Occipital Ctx	74.7
		Control 3 Occipital	
AD 4 Temporal Ctx	15.8	Control (Path) 1	47.3

		Occipital Ctx	
AD 5 Inf Temporal Ctx	92.0	Control (Path) 2 Occipital Ctx	13.5
AD 5 Sup Temporal Ctx	43.2	Control (Path) 3 Occipital Ctx	4.1
AD 6 Inf Temporal Ctx	26.4	Control (Path) 4 Occipital Ctx	14.6
AD 6 Sup Temporal Ctx	31.6	Control 1 Parietal Ctx	7.6
Control 1 Temporal Ctx	5.8	Control 2 Parietal Ctx	39.2
Control 2 Temporal Ctx	51.8	Control 3 Parietal Ctx	21.9
Control 3 Temporal Ctx	14.5	Control (Path) 1 Parietal Ctx	56.3
Control 3 Temporal Ctx	8.1	Control (Path) 2 Parietal Ctx	20.2
Control (Path) 1 Temporal Ctx	39.2	Control (Path) 3 Parietal Ctx	6.2
Control (Path) 2 Temporal Ctx	40.9	Control (Path) 4 Parietal Ctx	24.5

Table PC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3333, Run 216516940	Tissue Name	Rel. Exp.(%) Ag3333, Run 216516940
Adipose	4.4	Renal ca. TK-10	40.1
Melanoma* Hs688(A).T	0.9	Bladder	5.0
Melanoma* Hs688(B).T	1.8	Gastric ca. (liver met.) NCI-N87	4.5
Melanoma* M14	2.7	Gastric ca. KATO III	20.0
Melanoma* LOXIMVI	0.3	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.9	Colon ca. SW480	100.0
Squamous cell carcinoma SCC-4	0.1	Colon ca. * (SW480 met) SW620	33.0
Testis Pool	2.1	Colon ca. HT29	5.0
Prostate ca. * (bone met) PC-3	2.4	Colon ca. HCT-116	0.1
Uterus Pool	0.5	Colon ca. SW1116	10.2
Ovarian ca.	52.9	Colon ca. Colo-205	0.2

OVCAR-3			
Ovarian ca. SK-OV-3	0.6	Colon ca. SW-48	0.2
Ovarian ca. OVCAR-4	17.9	Colon Pool	2.2
Ovarian ca. OVCAR-5	4.5	Small Intestine Pool	1.0
Ovarian ca. IGROV-1	0.9	Stomach Pool	0.9
Ovarian ca. OVCAR-8	15.4	Bone Marrow Pool	1.8
Ovary	4.2	Fetal Heart	10.9
Breast ca. MCF-7	0.7	Heart Pool	2.8
Breast ca. MDA-MB-231	0.4	Lymph Node Pool	4.4
Breast ca. BT 549	42.0	Fetal Skeletal Muscle	1.1
Breast ca. T47D	13.0	Skeletal Muscle Pool	46.7
Breast ca. MDA-N	0.1	Spleen Pool	0.0
Breast Pool	2.4	Thymus Pool	2.3
Trachea	2.4	CNS cancer (glio/astro) U87-MG	0.9
Lung	0.2	CNS cancer (glio/astro) U-118-MG	0.3
Fetal Lung	0.9	CNS cancer (neuro;met) SK-N-AS	69.7
Lung ca. NCI-N417	17.1	CNS cancer (astro) SF-539	2.2
Lung ca. LX-1	1.1	CNS cancer (astro) SNB-75	15.9
Lung ca. NCI-H146	14.5	CNS cancer (glio) SNB-19	0.6
Lung ca. SHP-77	37.6	CNS cancer (glio) SF-295	6.0
Lung ca. A549	0.4	Brain (Amygdala) Pool	28.5
Lung ca. NCI-H526	23.5	Brain (cerebellum)	29.1
Lung ca. NCI-H23	8.2	Brain (fetal)	21.3
Lung ca. NCI-H460	14.3	Brain (Hippocampus) Pool	27.7
Lung ca. HOP-62	1.7	Cerebral Cortex Pool	36.1
Lung ca. NCI-H522	86.5	Brain (Substantia nigra)	40.1
Fetal Liver		Brain (whole)	
Liver ca. HepG2	6.2	Spinal Cord Pool	12.3

Kidney Pool	3.8	Adrenal Gland	4.7
Fetal Kidney	7.4	Pituitary gland Pool	3.7
Renal ca. 786-0	0.2	Salivary Gland	48.0
Renal ca. A498	20.9	Thyroid (female)	1.1
Renal ca. ACHN	8.5	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	3.0	Pancreas Pool	4.0

Table PD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3333, Run 165084139	Tissue Name	Rel. Exp.(%) Ag3333, Run 165084139
Secondary Th1 act	0.8	HUVEC IL-1beta	0.0
Secondary Th2 act	3.0	HUVEC IFN gamma	0.5
Secondary Tr1 act	0.6	HUVEC TNF alpha + IFN gamma	0.8
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.5	HUVEC IL-11	0.3
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.6
Primary Th1 act	5.7	Lung Microvascular EC TNFalpha + IL-1beta	0.4
Primary Th2 act	9.8	Microvascular Dermal EC none	0.0
Primary Tr1 act	3.8	Microvascular Dermal EC TNFalpha + IL-1beta	0.4
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	1.1
Primary Th2 rest	0.4	Small airway epithelium none	1.9
Primary Tr1 rest	0.6	Small airway epithelium TNFalpha + IL-1beta	1.4
CD45RA CD4 lymphocyte act	4.1	Coronary artery SMC rest	1.7
CD45RO CD4 lymphocyte act	1.7	Coronary artery SMC TNFalpha + IL-1beta	1.2
CD8 lymphocyte act	1.4	Astrocytes rest	100.0
Secondary CD8 lymphocyte rest	7.4	Astrocytes TNFalpha + IL-1beta	59.9
Secondary CD8	0.0	KU 812 (Basophil) rest	2.0
Secondary Th1 Th2 Tr1 anti- CD1106 (Keratinocytes)	0.5	CD1106 (Keratinocytes)	12.5

CD95 CH11		none	
LAK cells rest	0.5	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	6.2
LAK cells IL-2	0.3	Liver cirrhosis	0.9
LAK cells IL-2+IL-12	0.5	Lupus kidney	3.9
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	29.3
LAK cells IL-2+ IL-18	0.6	NCI-H292 IL-4	39.5
LAK cells PMA/ionomycin	0.3	NCI-H292 IL-9	23.3
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	21.9
Two Way MLR 3 day	0.8	NCI-H292 IFN gamma	14.5
Two Way MLR 5 day	0.9	HPAEC none	0.5
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	4.5
PBMC PWM	8.1	Lung fibroblast TNF alpha + IL-1 beta	2.2
PBMC PHA-L	11.6	Lung fibroblast IL-4	12.9
Ramos (B cell) none	0.0	Lung fibroblast IL-9	9.2
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	8.5
B lymphocytes PWM	15.4	Lung fibroblast IFN gamma	8.4
B lymphocytes CD40L and IL-4	2.1	Dermal fibroblast CCD1070 rest	40.6
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	20.9
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	19.3
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	1.8
Dendritic cells LPS	0.5	Dermal fibroblast IL-4	3.8
Dendritic cells anti- CD40	0.0	IBD Colitis 2	0.0
Monocytes rest	0.0	IBD Crohn's	2.5
Monocytes LPS	0.0	Colon	4.2
Macrophages rest	0.0	Lung	9.1
Macrophages LPS	0.0	Thymus	11.3
HUVEC none	0.4	Kidney	2.6

NS_{neurodegeneration} V1.0 Summary: This panel confirms the expression of this gene in the brain in an independent group of individuals. However, no differential expression of this

gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3333 This gene is expressed at moderate to low levels in many of the samples on this panel, with the highest expression in colon cancer cell line SW480 (CT=27.8). Expression is significantly lower in SW680, a cell line derived from a metastasis of the primary tumor represented by SW480. Thus, expression of this gene could be used to differentiate between these two cell lines and potentially between primary colon cancer and its metastases.

Based on expression in this panel, this gene may be involved in gastric, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes

This gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3333 The CG57789-01 gene is expressed at moderate to low levels in several samples on this panel, with the highest expression in resting astrocytes (CT=28.4). Moderate expression of this gene is seen in treated and untreated dermal and lung fibroblasts and the airway epithelial tumor line NCI-H292 cells. Thus, the transcript or the protein it encodes may be involved in pathological and inflammatory skin and lung conditions,

CG57758-01 and CG57758-02: SODIUM LITHIUM-DEPENDENT
DICARBOXYLATE TRANSPORTER

Expression of gene CG57758-01, a splice variant of CG57758-02, and CG57758-02 was assessed using the primer-probe sets Ag3326 and Ag3692, described in Tables QA and QB. Results of the RTQ-PCR runs are shown in Tables QC, QD, QE and QF.

Table QA. Probe Name Ag3326

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccatttactggtgcacagaagt-3'	22	149	432
Probe	TET-5'-atccctctggctgtcacctctctcat-3'-TAMRA	26	172	433
Reverse	5'-ggagtccagaatctggaagagt-3'	22	216	434

Table QB. Probe Name Ag3692

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccatttactggtgcacagaagt-3'	22	149	435
Probe	TET-5'-atccctctggctgtcacctctctcat-3'-TAMRA	26	172	436
Reverse	5'-ggagtccagaatctggaagagt-3'	22	216	437

Table QC. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3326, Run 210144197	Rel. Exp.(%) Ag3692, Run 211145262	Rel. Exp.(%) Ag3692, Run 224337942	Tissue Name	Rel. Exp.(%) Ag3326, Run 210144197	Rel. Exp.(%) Ag3692, Run 211145262	Rel. Exp.(%) Ag3692, Run 224337942
AD 1 Hippo	2.1	4.3	1.0	Control (Path) 3 Temporal Ctx	8.5	15.3	12.0
AD 2 Hippo	20.9	28.3	25.0	Control (Path) 4 Temporal Ctx	31.2	36.6	52.1

AD 4	2.1	7.1	2.6	AD 2	0.0	0.0	0.0
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Hippo				Occipital Ctx (Missing)			
AD 5 hippo	72.7	97.9	85.3	AD 3 Occipital Ctx	1.5	7.2	1.3
AD 6 Hippo	13.7	18.3	5.5	AD 4 Occipital Ctx	71.7	35.6	30.6
Control 2 Hippo	14.5	20.2	15.2	AD 5 Occipital Ctx	25.3	31.9	12.4
Control 4 Hippo	11.7	7.4	5.1	AD 6 Occipital Ctx	17.2	19.1	11.2
Control (Path) 3 Hippo	6.7	4.4	4.5	Control 1 Occipital Ctx	7.0	9.0	8.1
AD 1 Temporal Ctx	4.0	1.7	2.8	Control 2 Occipital Ctx	33.2	44.8	26.1
AD 2 Temporal Ctx	80.7	50.7	37.4	Control 3 Occipital Ctx	30.1	37.6	21.9
AD 3 Temporal Ctx	3.6	0.0	1.1	Control 4 Occipital Ctx	16.3	12.6	8.2
AD 4 Temporal Ctx	19.5	30.6	15.2	Control (Path) 1 Occipital Ctx	42.0	55.9	52.9
AD 5 Inf Temporal Ctx	100.0	100.0	99.3	Control (Path) 2 Occipital Ctx	6.7	13.0	7.7
AD 5 SupTemp oral Ctx	32.8	29.1	33.2	Control (Path) 3 Occipital Ctx	8.7	6.6	5.4
Temporal Ctx				Occipital Ctx			

AD 6 Sup Temporal Ctx	41.8	53.6	17.0	Control 1 Parietal Ctx	21.2	23.0	15.3
Control 1 Temporal Ctx	12.0	33.9	18.3	Control 2 Parietal Ctx	48.6	38.2	22.1
Control 2 Temporal Ctx	30.1	49.3	44.4	Control 3 Parietal Ctx	28.3	34.4	32.8
Control 3 Temporal Ctx	38.7	39.5	33.4	Control (Path) 1 Parietal Ctx	78.5	97.3	100.0
Control 4 Temporal Ctx	17.6	25.2	24.1	Control (Path) 2 Parietal Ctx	50.7	50.7	37.9
Control (Path) 1 Temporal Ctx	69.7	70.7	49.7	Control (Path) 3 Parietal Ctx	10.7	10.1	9.6
Control (Path) 2 Temporal Ctx	35.4	50.7	33.4	Control (Path) 4 Parietal Ctx	30.6	24.5	40.9

Table QD. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3326, Run 215678613	Rel. Exp.(%) Ag3692, Run 217131191	Tissue Name	Rel. Exp.(%) Ag3326, Run 215678613	Rel. Exp.(%) Ag3692, Run 217131191
Adipose	0.0	0.0	Renal ca. TK-10	11.4	12.0
Melanoma* Hs688(A).T	0.0	0.0	Bladder	0.0	0.1
Melanoma* Hs688(B).T	0.1	0.0	Gastric ca. (liver met.) NCI-N87	0.0	0.0
Melanoma* M14	0.0	0.0	Gastric ca. KATO III	0.0	0.0
Melanoma* LOXIMVI	0.0	0.0	Colon ca. SW- 648	0.0	0.0
Squamous cell carcinoma	0.0	0.0	Colon ca. * (SW480 met)	0.0	0.0

SCC-4			SW620		
Testis Pool	0.1	0.2	Colon ca. HT29	0.0	0.0
Prostate ca.* (bone met) PC-3	0.0	0.0	Colon ca. HCT-116	0.0	0.0
Prostate Pool	0.0	0.0	Colon ca. CaCo-2	0.0	0.0
Placenta	0.0	0.0	Colon cancer tissue	0.1	0.0
Uterus Pool	0.0	0.0	Colon ca. SW1116	0.0	0.0
Ovarian ca. OVCAR-3	0.0	0.0	Colon ca. Colo-205	0.0	0.0
Ovarian ca. SK-OV-3	0.0	0.0	Colon ca. SW-48	0.0	0.0
Ovarian ca. OVCAR-4	0.1	0.0	Colon Pool	0.6	0.0
Ovarian ca. OVCAR-5	0.0	0.0	Small Intestine Pool	0.1	0.0
Ovarian ca. IGROV-1	0.0	0.0	Stomach Pool	0.0	0.0
Ovarian ca. OVCAR-8	2.8	2.2	Bone Marrow Pool	0.0	0.1
Ovary	0.7	0.6	Fetal Heart	0.0	0.0
Breast ca. MCF-7	0.0	0.0	Heart Pool	0.0	0.0
Breast ca. MDA-MB-231	0.0	0.0	Lymph Node Pool	0.1	0.0
Breast ca. BT 549	0.6	0.8	Fetal Skeletal Muscle	0.0	0.0
Breast ca. T47D	0.0	0.0	Skeletal Muscle Pool	0.0	0.0
Breast ca. MDA-N	0.0	0.0	Spleen Pool	0.4	0.2
Breast Pool	0.0	0.1	Thymus Pool	0.0	0.0
Trachea	0.2	0.1	CNS cancer (glio/astro) U87-MG	0.0	0.0
Lung	0.0	0.0	CNS cancer (glio/astro) U-118-MG	0.0	0.0
Lung ca. NCI-N417	0.0	0.0	CNS cancer (astro) SF-539	0.0	0.0

Lung ca. LX-1	0.0	0.0	CNS cancer (astro) SNB-75	0.0	0.0
Lung ca. NCI-H146	0.0	0.0	CNS cancer (glio) SNB-19	0.0	0.0
Lung ca. SHP-77	0.0	0.0	CNS cancer (glio) SF-295	0.1	0.1
Lung ca. A549	0.0	0.1	Brain (Amygdala) Pool	0.4	0.4
Lung ca. NCI-H526	2.0	0.0	Brain (cerebellum)	1.4	1.0
Lung ca. NCI-H23	0.7	0.6	Brain (fetal)	0.7	0.4
Lung ca. NCI-H460	0.0	0.0	Brain (Hippocampus) Pool	0.5	0.7
Lung ca. HOP-62	0.1	0.2	Cerebral Cortex Pool	1.4	1.5
Lung ca. NCI-H522	0.0	0.0	Brain (Substantia nigra) Pool	1.4	1.4
Liver	28.7	24.1	Brain (Thalamus) Pool	1.1	0.9
Fetal Liver	100.0	100.0	Brain (whole)	4.1	3.7
Liver ca. HepG2	29.5	26.2	Spinal Cord Pool	0.1	0.2
Kidney Pool	0.0	0.0	Adrenal Gland	2.6	1.9
Fetal Kidney	0.1	0.1	Pituitary gland Pool	0.0	0.2
Renal ca. 786-0	0.0	0.0	Salivary Gland	40.9	35.1
Renal ca. A498	0.0	0.0	Thyroid (female)	0.0	0.0
Renal ca. ACHN	0.0	0.0	Pancreatic ca. CAPAN2	0.5	0.8
Renal ca. UO-31	0.0	0.0	Pancreas Pool	0.0	0.0

Table QE. Panel 4.1D

Tissue Name	Rel. Exp.(%) Ag3692, Run 169987356	Tissue Name	Rel. Exp.(%) Ag3692, Run 169987356
Secondary T cell act	0.0	SPV ECTINE alpha + beta gamma	0.0

Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	11.3
Primary Tr1 act	4.2	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	28.5
Primary Th2 rest	0.0	Small airway epithelium none	5.7
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	3.9	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	3.6
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	4.3
2ry Th1/Th2/Tr1 _anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	10.7
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	94.0
LAK cells IL-2+IL-12	0.0	NCI-H292 none	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 IL-4	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-9	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-13	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 3 day	0.0	HPAEC none	0.0
		HPAEC TNF alpha + IL-1	
PBMC rest	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0

PBMC PWM	0.0	Lung fibroblast IL-4	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-13	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes PWM	0.0	Dermal fibroblast CCD1070 rest	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells none	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells LPS	0.0	Dermal Fibroblasts rest	0.0
Dendritic cells anti-CD40	0.0	Neutrophils TNF α +LPS	0.0
Monocytes rest	0.0	Neutrophils rest	0.0
Monocytes LPS	0.0	Colon	0.0
Macrophages rest	0.0	Lung	0.0
Macrophages LPS	0.0	Thymus	2.4
HUVEC none	0.0	Kidney	100.0
HUVEC starved	0.0		

Table QF. Panel 5 Islet

Tissue Name	Rel. Exp.(%) Ag3326, Run 242385365	Tissue Name	Rel. Exp.(%) Ag3326, Run 242385365
97457_Patient-02go_adipose	0.0	94709_Donor 2 AM - A_adipose	0.2
97476_Patient-07sk_skeletal muscle	0.0	94710_Donor 2 AM - B_adipose	0.0
97477_Patient-07ut_uterus	0.0	94711_Donor 2 AM - C_adipose	0.0
97478_Patient-07pl_placenta	0.0	94712_Donor 2 AD - A_adipose	0.0
99167_Bayer Patient 1	0.3	94713_Donor 2 AD - B_adipose	0.0
97482_Patient-08ut_uterus	0.0	94714_Donor 2 AD - C_adipose	0.0

97486_Patient-09sk_skeletal muscle

97488_Donor 2 B_Mesenchymal Stem Cells

97487_Patient-09ut_uterus	0.0	94730_Donor 3 AM - A_adipose	0.0
97488_Patient-09pl_placenta	0.0	94731_Donor 3 AM - B_adipose	0.0
97492_Patient-10ut_uterus	0.0	94732_Donor 3 AM - C_adipose	0.0
97493_Patient-10pl_placenta	0.0	94733_Donor 3 AD - A_adipose	0.0
97495_Patient-11go_adipose	0.0	94734_Donor 3 AD - B_adipose	0.0
97496_Patient-11sk_skeletal muscle	0.0	94735_Donor 3 AD - C_adipose	0.0
97497_Patient-11ut_uterus	0.0	77138_Liver_HepG2untreated	100.0
97498_Patient-11pl_placenta	0.0	73556_Heart_Cardiac stromal cells (primary)	0.0
97500_Patient-12go_adipose	0.1	81735_Small Intestine	39.5
97501_Patient-12sk_skeletal muscle	0.3	72409_Kidney_Proximal Convoluted Tubule	0.0
97502_Patient-12ut_uterus	0.0	82685_Small intestine_Duodenum	0.0
97503_Patient-12pl_placenta	0.0	90650_Adrenal_Adrenocortical adenoma	0.0
94721_Donor 2 U - A_Mesenchymal Stem Cells	0.0	72410_Kidney_HRCE	0.0
94722_Donor 2 U - B_Mesenchymal Stem Cells	0.0	72411_Kidney_HRE	0.0
94723_Donor 2 U - C_Mesenchymal Stem Cells	0.0	73139_Uterus_Uterine smooth muscle cells	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3326/Ag3692 - Three experiments done with two primer pairs (same sequence) are in excellent agreement. This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system

General_screening_panel_v1.4 Summary: Ag3326/Ag3692 Two experiments with the smac probe and primer set produce results that are in excellent agreement. This gene is highly expressed in fetal liver (CT=26.5-27.0) and moderately expressed in adult liver (CT=28.5-28.8) and liver cancer cell line HepG2 (CT=28.4-28.8). This result agrees with the results seen in Panel 5 (expression in HepG2 (CT=29.2). These results are in agreement with published data that show a novel sodium dicarboxylate transporter in brain, choroid plexus kidney, intestine and liver. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker for liver derived tissue.

This gene is expressed at low levels throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, and cerebral cortex. Therefore, this gene may play a role in central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Low but significant levels of expression are also seen in the adrenal gland. Thus, this gene product may also be involved in metabolic disorders of this gland, including adrenoleukodystrophy and congenital adrenal hyperplasia.

References:

1. Pajor AM, Gangula R, Yao X. Cloning and functional characterization of a high-affinity Na(+)/dicarboxylate cotransporter from mouse brain. *Am J Physiol Cell Physiol* 2001 May;280(5):C1215-23.
2. Chen XZ, Shayakul C, Berger UV, Tian W, Hediger MA. Characterization of a rat Na+-dicarboxylate cotransporter. *J Biol Chem* 1998 Aug 14;273(33):20972-81.

Panel 4.1D Summary: Ag3692 Significant expression of this gene is seen only in kidney and a liver cirrhosis sample (CTs=34.0). These results confirm that this gene is expressed in liver derived samples. The presence in the kidney is also in agreement with published results. Please see Panel 1.4. This gene product may be involved in maintaining or restoring normal function to the kidney during inflammation.

Panel 5 Islet Summary: Ag3326 - The highest expression of this gene is in liver cancer cell line HepG2 (CT=29.2). There is also moderate expression in the small intestine (CT=30.5). These results compare well with previously published reports of sodium dicarboxylate transporter expression in mouse and rat (see discussion Panel 1.4).

R. CG57758-04 and CG57758-05: Sodium:sulfate symporter

Expression of gene CG57758-04 and CG57758-05, both splice variants of CG577584-01, was assessed using the primer-probe sets Ag3326, Ag3692 and Ag5818, described in Tables RA, RB and RC. Results of the RTQ-PCR runs are shown in Tables RD, RE, RF, RG and RH.

Table RA. Probe Name Ag3326

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccatttactggtgcacagaagt-3'	22	138	438
Probe	TET-5'-atccctctggctgtcacctctctcat-3'-TAMRA	26	161	439
Reverse	5'-ggagtccagaatctggaagagt-3'	22	205	440

Table RB. Probe Name Ag3692

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccatttactggtgcacagaagt-3'	22	138	441
Probe	TET-5'-atccctctggctgtcacctctctcat-3'-TAMRA	26	161	442
Reverse	5'-ggagtccagaatctggaagagt-3'	22	205	443

Table RC. Probe Name Ag5818

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccatcaccttgatcttgtcc-3'	20	1341	444
Probe	TET-5'-ttatgactcctgttttcaccatggaggca-3'-TAMRA	29	1429	445
Reverse	5'-cagaagactccaattatgttca-3'	22	1458	446

Tissue Name	Rel. Exp.(%)	Rel. Exp.(%)	Rel. Exp.(%)	Tissue Name	Rel. Exp.(%)	Rel. Exp.(%)	Rel. Exp.(%)
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	Ag3326, Run 210144197	Ag3692, Run 211145262	Ag3692, Run 224337942		Ag3326, Run 210144197	Ag3692, Run 211145262	Ag3692, Run 224337942
AD 1 Hippo	2.1	4.3	1.0	Control (Path) 3 Tempora l Ctx	8.5	15.3	12.0
AD 2 Hippo	20.9	28.3	25.0	Control (Path) 4 Tempora l Ctx	31.2	36.6	52.1
AD 3 Hippo	0.0	0.9	0.6	AD 1 Occipital Ctx	2.7	3.0	0.0
AD 4 Hippo	2.1	7.1	2.6	AD 2 Occipital Ctx (Missing)	0.0	0.0	0.0
AD 5 hippo	72.7	97.9	85.3	AD 3 Occipital Ctx	1.5	7.2	1.3
AD 6 Hippo	13.7	18.3	5.5	AD 4 Occipital Ctx	71.7	35.6	30.6
Control 2 Hippo	14.5	20.2	15.2	AD 5 Occipital Ctx	25.3	31.9	12.4
Control 4 Hippo	11.7	7.4	5.1	AD 6 Occipital Ctx	17.2	19.1	11.2
Control (Path) 3 Hippo	6.7	4.4	4.5	Control 1 Occipital Ctx	7.0	9.0	8.1
AD 1 Temporal Ctx	4.0	1.7	2.8	Control 2 Occipital Ctx	33.2	44.8	26.1
AD 2 Temporal Ctx	80.7	50.7	37.4	Control 3 Occipital Ctx	30.1	37.6	21.9

AD 4	19.5	30.6	15.2	Control	42.0	55.9	52.9
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Temporal Ctx				(Path) 1 Occipital Ctx			
AD 5 Inf Temporal Ctx	100.0	100.0	99.3	Control (Path) 2 Occipital Ctx	6.7	13.0	7.7
AD 5 Sup Temporal Ctx	32.8	29.1	33.2	Control (Path) 3 Occipital Ctx	8.7	6.6	5.4
AD 6 Inf Temporal Ctx	27.7	21.3	26.6	Control (Path) 4 Occipital Ctx	8.1	9.0	7.4
AD 6 Sup Temporal Ctx	41.8	53.6	17.0	Control 1 Parietal Ctx	21.2	23.0	15.3
Control 1 Temporal Ctx	12.0	33.9	18.3	Control 2 Parietal Ctx	48.6	38.2	22.1
Control 2 Temporal Ctx	30.1	49.3	44.4	Control 3 Parietal Ctx	28.3	34.4	32.8
Control 3 Temporal Ctx	38.7	39.5	33.4	Control (Path) 1 Parietal Ctx	78.5	97.3	100.0
Control 4 Temporal Ctx	17.6	25.2	24.1	Control (Path) 2 Parietal Ctx	50.7	50.7	37.9
Control (Path) 1 Temporal Ctx	69.7	70.7	49.7	Control (Path) 3 Parietal Ctx	10.7	10.1	9.6
Control (Path) 2 Temporal Ctx	35.4	50.7	33.4	Control (Path) 4 Parietal Ctx	30.6	24.5	40.9

Tissue Name	Rel. Exp.(%)	Rel. Exp.(%)	Tissue Name	Rel. Exp.(%)	Rel. Exp.(%)
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	Ag3326, Run 215678613	Ag3692, Run 217131191		Ag3326, Run 215678613	Ag3692, Run 217131191
Adipose	0.0	0.0	Renal ca. TK-10	11.4	12.0
Melanoma* Hs688(A).T	0.0	0.0	Bladder	0.0	0.1
Melanoma* Hs688(B).T	0.1	0.0	Gastric ca. (liver met.) NCI-N87	0.0	0.0
Melanoma* M14	0.0	0.0	Gastric ca. KATO III	0.0	0.0
Melanoma* LOXIMVI	0.0	0.0	Colon ca. SW- 948	0.0	0.0
Melanoma* SK-MEL-5	0.0	0.0	Colon ca. SW480	0.0	0.0
Squamous cell carcinoma SCC-4	0.9	0.7	Colon ca.* (SW480 met) SW620	0.0	0.0
Testis Pool	0.1	0.2	Colon ca. HT29	0.0	0.0
Prostate ca.* (bone met) PC-3	0.0	0.0	Colon ca. HCT- 116	0.0	0.0
Prostate Pool	0.0	0.0	Colon ca. CaCo-2	0.0	0.0
Placenta	0.0	0.0	Colon cancer tissue	0.1	0.0
Uterus Pool	0.0	0.0	Colon ca. SW1116	0.0	0.0
Ovarian ca. OVCAR-3	0.0	0.0	Colon ca. Colo- 205	0.0	0.0
Ovarian ca. SK-OV-3	0.0	0.0	Colon ca. SW-48	0.0	0.0
Ovarian ca. OVCAR-4	0.1	0.0	Colon Pool	0.6	0.0
Ovarian ca. OVCAR-5	0.0	0.0	Small Intestine Pool	0.1	0.0
Ovarian ca. IGROV-1	0.0	0.0	Stomach Pool	0.0	0.0
Ovarian ca. OVCAR-8	2.8	2.2	Bone Marrow Pool	0.0	0.1
Ovary	0.7	0.6	Fetal Heart	0.0	0.0
Breast ca. MCF-7	0.0	0.0	Heart Pool	0.0	0.0
Breast ca. MCF-10A			Lymph Node		
Brain			Muscle		

Breast ca. T47D	0.0	0.0	Skeletal Muscle Pool	0.0	0.0
Breast ca. MDA-N	0.0	0.0	Spleen Pool	0.4	0.2
Breast Pool	0.0	0.1	Thymus Pool	0.0	0.0
Trachea	0.2	0.1	CNS cancer (glio/astro) U87-MG	0.0	0.0
Lung	0.0	0.0	CNS cancer (glio/astro) U-118-MG	0.0	0.0
Fetal Lung	0.2	0.1	CNS cancer (neuro;met) SK-N-AS	0.0	0.0
Lung ca. NCI-N417	0.0	0.0	CNS cancer (astro) SF-539	0.0	0.0
Lung ca. LX-1	0.0	0.0	CNS cancer (astro) SNB-75	0.0	0.0
Lung ca. NCI-H146	0.0	0.0	CNS cancer (glio) SNB-19	0.0	0.0
Lung ca. SHP-77	0.0	0.0	CNS cancer (glio) SF-295	0.1	0.1
Lung ca. A549	0.0	0.1	Brain (Amygdala) Pool	0.4	0.4
Lung ca. NCI-H526	2.0	0.0	Brain (cerebellum)	1.4	1.0
Lung ca. NCI-H23	0.7	0.6	Brain (fetal)	0.7	0.4
Lung ca. NCI-H460	0.0	0.0	Brain (Hippocampus) Pool	0.5	0.7
Lung ca. HOP-62	0.1	0.2	Cerebral Cortex Pool	1.4	1.5
Lung ca. NCI-H522	0.0	0.0	Brain (Substantia nigra) Pool	1.4	1.4
Liver	28.7	24.1	Brain (Thalamus) Pool	1.1	0.9
Fetal Liver	100.0	100.0	Brain (whole)	4.1	3.7
Liver ca. HepG2	29.5	26.2	Spinal Cord Pool	0.1	0.2
Kidney Pool	0.0	0.0	Adrenal Gland	2.6	1.9
			Pituitary gland		

SURVIVAL CURVES

Renal ca.	0.0	0.0	Thyroid (female)	0.0	0.0
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A498					
Renal ca. ACHN	0.0	0.0	Pancreatic ca. CAPAN2	0.5	0.8
Renal ca. UO-31	0.0	0.0	Pancreas Pool	0.0	0.0

Table RF. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag5818, Run 245382899	Tissue Name	Rel. Exp.(%) Ag5818, Run 245382899
Adipose	0.0	Renal ca. TK-10	13.4
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	1.4	Colon ca. * (SW480 met) SW620	0.0
Testis Pool	0.5	Colon ca. HT29	0.0
Prostate ca. * (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.4
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.1	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	1.9	Bone Marrow Pool	0.0
Ovary	0.3	Fetal Heart	0.0

MB-231

lymph. Node Pool

Breast ca. BT 549	0.4	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.7
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.2	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.2	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF- 295	0.0
Lung ca. A549	0.2	Brain (Amygdala) Pool	0.7
Lung ca. NCI-H526	0.0	Brain (cerebellum)	1.1
Lung ca. NCI-H23	1.5	Brain (fetal)	0.8
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.6
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	1.7
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	1.2
Liver	40.3	Brain (Thalamus) Pool	1.3
Fetal Liver	100.0	Brain (whole)	5.6
Liver ca. HepG2	33.2	Spinal Cord Pool	0.3
Kidney Pool	0.0	Adrenal Gland	6.0
Fetal Kidney	0.0	Pituitary gland Pool	0.2
Renal ca. 786-0	0.0	Salivary Gland	67.4
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.7
Renal ca. UO-31	0.0	Pancreas Pool	0.0

Table RG. Panel 4.1D

	Rel. Exp (%)	Rel. Exp (%)		Rel. Exp. (%)	Rel. Exp. (%)
	169987356	246920287		169987356	246920287
Secondary Th1 act	0.0	0.0	HUVEC IL-1beta	0.0	0.0

Secondary Th2 act	0.0	0.0	HUVEC IFN gamma	0.0	0.0
Secondary Tr1 act	0.0	0.0	HUVEC TNF alpha + IFN gamma	0.0	0.0
Secondary Th1 rest	0.0	0.0	HUVEC TNF alpha + IL4	0.0	0.0
Secondary Th2 rest	0.0	0.0	HUVEC IL-11	0.0	0.0
Secondary Tr1 rest	0.0	0.0	Lung Microvascular EC none	0.0	0.0
Primary Th1 act	0.0	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0	0.0
Primary Th2 act	0.0	0.0	Microvascular Dermal EC none	11.3	0.0
Primary Tr1 act	4.2	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0	0.0
Primary Th1 rest	0.0	0.0	Bronchial epithelium TNFalpha + IL1beta	28.5	0.0
Primary Th2 rest	0.0	0.0	Small airway epithelium none	5.7	0.0
Primary Tr1 rest	0.0	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0	0.0
CD45RA CD4 lymphocyte act	3.9	0.0	Coronary artery SMC rest	0.0	0.0
CD45RO CD4 lymphocyte act	0.0	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0	0.0
CD8 lymphocyte act	0.0	0.0	Astrocytes rest	0.0	0.0
Secondary CD8 lymphocyte rest	0.0	0.0	Astrocytes TNFalpha + IL-1beta	0.0	0.0
Secondary CD8 lymphocyte act	0.0	0.0	KU-812 (Basophil) rest	3.6	24.3
2ry	0.0	0.0	CCD1106	10.7	0.0

Th1/Th2/Tr1 anti-CD95 CH11			(Keratinocytes) none		
LAK cells rest	0.0	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0	0.0
LAK cells IL-2	0.0	0.0	Liver cirrhosis	94.0	27.5
LAK cells IL-2+IL-12	0.0	0.0	NCI-H292 none	0.0	0.0
LAK cells IL-2+IFN gamma	0.0	0.0	NCI-H292 IL-4	0.0	0.0
LAK cells IL-2+IL-18	0.0	0.0	NCI-H292 IL-9	0.0	0.0
LAK cells PMA/ionomycin	0.0	0.0	NCI-H292 IL-13	0.0	0.0
NK Cells IL-2 rest	0.0	0.0	NCI-H292 IFN gamma	0.0	0.0
Two Way MLR 3 day	0.0	0.0	HPAEC none	0.0	0.0
Two Way MLR 5 day	3.2	0.0	HPAEC TNF alpha + IL-1 beta	0.0	0.0
Two Way MLR 7 day	0.0	0.0	Lung fibroblast none	0.0	0.0
PBMC rest	0.0	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0	0.0
PBMC PWM	0.0	0.0	Lung fibroblast IL-4	0.0	0.0
PBMC PHA-L	0.0	0.0	Lung fibroblast IL-9	0.0	0.0
Ramos (B cell) none	0.0	0.0	Lung fibroblast IL-13	0.0	0.0
Ramos (B cell) ionomycin	0.0	0.0	Lung fibroblast IFN gamma	0.0	0.0
B lymphocytes PWM	0.0	0.0	Dermal fibroblast CCD1070 rest	0.0	0.0
B lymphocytes CD40L and IL-4	0.0	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0	0.0
EOL-1 dbcAMP	0.0	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0	0.0
Dendritic cells none	0.0	0.0	Dermal fibroblast IL-4	0.0	0.0

Dendritic cells LPS	0.0	0.0	Dermal Fibroblasts rest	0.0	0.0
Dendritic cells anti-CD40	0.0	0.0	Neutrophils TNFa+LPS	0.0	0.0
Monocytes rest	0.0	0.0	Neutrophils rest	0.0	0.0
Monocytes LPS	0.0	0.0	Colon	0.0	0.0
Macrophages rest	0.0	0.0	Lung	0.0	0.0
Macrophages LPS	0.0	0.0	Thymus	2.4	0.0
HUVEC none	0.0	0.0	Kidney	100.0	100.0
HUVEC starved	0.0	0.0			

Table RH. Panel 5 Islet

Tissue Name	Rel. Exp.(%) Ag3326, Run 242385365	Tissue Name	Rel. Exp.(%) Ag3326, Run 242385365
97457_Patient-02go_adipose	0.0	94709_Donor 2 AM - A_adipose	0.2
97476_Patient-07sk_skeletal muscle	0.0	94710_Donor 2 AM - B_adipose	0.0
97477_Patient-07ut_uterus	0.0	94711_Donor 2 AM - C_adipose	0.0
97478_Patient-07pl_placenta	0.0	94712_Donor 2 AD - A_adipose	0.0
99167_Bayer Patient 1	0.3	94713_Donor 2 AD - B_adipose	0.0
97482_Patient-08ut_uterus	0.0	94714_Donor 2 AD - C_adipose	0.0
97483_Patient-08pl_placenta	0.0	94742_Donor 3 U - A_Mesenchymal Stem Cells	0.0
97486_Patient-09sk_skeletal muscle	0.0	94743_Donor 3 U - B_Mesenchymal Stem Cells	0.0
97487_Patient-09ut_uterus	0.0	94730_Donor 3 AM - A_adipose	0.0
97488_Patient-09pl_placenta	0.0	94731_Donor 3 AM - B_adipose	0.0
97492_Patient-10ut_uterus	0.0	94732_Donor 3 AM - C_adipose	0.0
97493_Patient-10pl_placenta	0.0	94733_Donor 3 AD - A_adipose	0.0
97495_Patient-11go_adipose	0.0	94734_Donor 3 AD - B_adipose	0.0
97497_Patient-11ut_uterus	0.0	77158_Liver HepG2untreated	100.0

97498_Patient-11pl_placenta	0.0	73556_Heart_Cardiac stromal cells (primary)	0.0
97500_Patient-12go_adipose	0.1	81735_Small Intestine	39.5
97501_Patient-12sk_skeletal muscle	0.3	72409_Kidney_Proximal Convoluted Tubule	0.0
97502_Patient-12ut_uterus	0.0	82685_Small intestine_Duodenum	0.0
97503_Patient-12pl_placenta	0.0	90650_Adrenal_Adrenocortical adenoma	0.0
94721_Donor 2 U - A_Mesenchymal Stem Cells	0.0	72410_Kidney_HRCE	0.0
94722_Donor 2 U - B_Mesenchymal Stem Cells	0.0	72411_Kidney_HRE	0.0
94723_Donor 2 U - C_Mesenchymal Stem Cells	0.0	73139_Uterus_Uterine smooth muscle cells	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3326/Ag3692 - Three experiments done with two primer pairs (same sequence) are in excellent agreement. This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders. Ag5818 Results from one experiment are not included. The amp plot indicates that there were experimental difficulties with this run.

General_screening_panel_v1.4 Summary: Ag3326/Ag3692 Two experiments with the same probe and primer set produce results that are in excellent agreement. This gene is highly expressed in fetal liver (CT=26.5-27.0) and moderately expressed in adult liver (CT=28.5-28.8) and liver cancer cell line HepG2 (CT=28.4-28.8). This result agrees with the results seen in Panel 5 (expression in HepG2 (CT=29.2). These results are in agreement with published data that show a novel sodium dicarboxylate transporter in brain, choroid plexus kidney, intestine and liver. Thus, expression of this gene could be used to differentiate between these tissues and other tissues on this panel and as a marker for liver derived tissue.

Ag3326/Ag3692 was also tested in a panel of tissues including substantia nigra, thalamus, cerebellum, and cerebral cortex. Therefore, this gene may play a

role in central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Low but significant levels of expression are also seen in the adrenal gland. Thus, this gene product may also be involved in metabolic disorders of this gland, including adrenoleukodystrophy and congenital adrenal hyperplasia.

References:

1. Pajor AM, Gangula R, Yao X. Cloning and functional characterization of a high-affinity Na(+)/dicarboxylate cotransporter from mouse brain. *Am J Physiol Cell Physiol* 2001 May;280(5):C1215-23.
2. Chen XZ, Shayakul C, Berger UV, Tian W, Hediger MA. Characterization of a rat Na+-dicarboxylate cotransporter. *J Biol Chem* 1998 Aug 14;273(33):20972-81.

General_screening_panel_v1.5 Summary: Ag5818 Results using this primer pair are in excellent agreement with the results seen in panel 1.4. See Panel 1.4 for discussion.

Panel 4.1D Summary: Ag3692 Significant expression of this gene is seen only in kidney and a liver cirrhosis sample (CTs=34.0). These results confirm that this gene is expressed in liver derived samples. The presence in the kidney is also in agreement with published results. Please see Panel 1.4. This gene product may be involved in maintaining or restoring normal function to the kidney during inflammation.

Panel 4D Summary: Ag3326 Results from one experiment are not included. The amp plot indicates that there were experimental difficulties with this run.

Panel 5 Islet Summary: Ag3326 The highest expression of this gene is in liver cancer cell line HepG2 (CT=29.2). There is also moderate expression in the small intestine (CT=30.5). These results compare well with previously published reports of sodium dicarboxylate transporter expression in mouse and rat (see discussion Panel 1.4).

S. CG57732-01 and CG57732-02 and CG57732-03: CA2+/CALMODULIN-

EXPRESSION OF CYCLO-OXYGENASE-2 (COX-2) IN RAT COLONIC EPITHELIAL CELLS
was assessed using the primer-probe set Ag3317, described in Table SA. Results of the RTQ-

PCR runs are shown in Tables SB, SC and SD. Please note CG57732-03 represents a splice variant of CG57732-01.

Table SA. Probe Name Ag3317

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ggcctacaacgaaagtgaaga-3'	21	451	447
Probe	TET-5'-cagacactatgcaatgaaagtcctttcca-3'-TAMRA	29	472	448
Reverse	5'-ggaaagccatactgcttcagta-3'	22	510	449

Table SB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3317, Run 210144081	Tissue Name	Rel. Exp.(%) Ag3317, Run 210144081
AD 1 Hippo	10.7	Control (Path) 3 Temporal Ctx	4.1
AD 2 Hippo	23.7	Control (Path) 4 Temporal Ctx	42.6
AD 3 Hippo	4.5	AD 1 Occipital Ctx	12.5
AD 4 Hippo	7.5	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	97.9	AD 3 Occipital Ctx	5.4
AD 6 Hippo	25.7	AD 4 Occipital Ctx	18.4
Control 2 Hippo	24.8	AD 5 Occipital Ctx	21.8
Control 4 Hippo	4.3	AD 6 Occipital Ctx	58.6
Control (Path) 3 Hippo	2.8	Control 1 Occipital Ctx	1.5
AD 1 Temporal Ctx	10.4	Control 2 Occipital Ctx	94.0
AD 2 Temporal Ctx	35.8	Control 3 Occipital Ctx	21.5
AD 3 Temporal Ctx	5.8	Control 4 Occipital Ctx	2.6
AD 4 Temporal Ctx	23.2	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	88.9	Control (Path) 2 Occipital Ctx	13.8

AD 6 Hippo
Ctx

Control (Path) 4
Occipital Ctx

AD 6 Sup Temporal Ctx	47.3	Control 1 Parietal Ctx	4.9
Control 1 Temporal Ctx	4.4	Control 2 Parietal Ctx	33.0
Control 2 Temporal Ctx	63.3	Control 3 Parietal Ctx	27.4
Control 3 Temporal Ctx	20.4	Control (Path) 1 Parietal Ctx	95.9
Control 4 Temporal Ctx	8.7	Control (Path) 2 Parietal Ctx	24.5
Control (Path) 1 Temporal Ctx	77.4	Control (Path) 3 Parietal Ctx	2.0
Control (Path) 2 Temporal Ctx	38.7	Control (Path) 4 Parietal Ctx	51.8

Table SC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3317, Run 215678602	Tissue Name	Rel. Exp.(%) Ag3317, Run 215678602
Adipose	2.4	Renal ca. TK-10	14.2
Melanoma* Hs688(A).T	6.2	Bladder	10.5
Melanoma* Hs688(B).T	7.9	Gastric ca. (liver met.) NCI-N87	22.2
Melanoma* M14	18.2	Gastric ca. KATO III	23.0
Melanoma* LOXIMVI	9.4	Colon ca. SW-948	11.1
Melanoma* SK-MEL-5	9.8	Colon ca. SW480	20.9
Squamous cell carcinoma SCC-4	1.6	Colon ca.* (SW480 met) SW620	21.6
Testis Pool	13.1	Colon ca. HT29	11.3
Prostate ca.* (bone met) PC-3	6.4	Colon ca. HCT-116	27.0
Prostate Pool	3.1	Colon ca. CaCo-2	1.6
Placenta	1.8	Colon cancer tissue	11.3
Uterus Pool	3.9	Colon ca. SW1116	9.7
Ovarian ca. OVCAR-3	11.6	Colon ca. Colo-205	1.7
Ovarian ca. SK-OV-3	18.7	Colon ca. SW-48	8.8
Ovarian ca. OVCAR-5	17.2	Small Intestine Pool	21.2

Ovarian ca. IGROV-1	6.2	Stomach Pool	5.3
Ovarian ca. OVCAR-8	4.7	Bone Marrow Pool	5.1
Ovary	2.9	Fetal Heart	6.8
Breast ca. MCF-7	6.1	Heart Pool	5.4
Breast ca. MDA-MB-231	20.3	Lymph Node Pool	13.4
Breast ca. BT 549	7.4	Fetal Skeletal Muscle	2.6
Breast ca. T47D	37.9	Skeletal Muscle Pool	2.3
Breast ca. MDA-N	9.0	Spleen Pool	2.8
Breast Pool	12.0	Thymus Pool	9.0
Trachea	17.2	CNS cancer (glio/astro) U87-MG	66.4
Lung	0.7	CNS cancer (glio/astro) U-118-MG	53.2
Fetal Lung	6.0	CNS cancer (neuro;met) SK-N-AS	4.6
Lung ca. NCI-N417	16.5	CNS cancer (astro) SF-539	17.2
Lung ca. LX-1	20.9	CNS cancer (astro) SNB-75	21.5
Lung ca. NCI-H146	7.0	CNS cancer (glio) SNB-19	5.1
Lung ca. SHP-77	23.0	CNS cancer (glio) SF-295	12.2
Lung ca. A549	23.7	Brain (Amygdala) Pool	46.3
Lung ca. NCI-H526	4.4	Brain (cerebellum)	92.7
Lung ca. NCI-H23	5.8	Brain (fetal)	25.7
Lung ca. NCI-H460	10.3	Brain (Hippocampus) Pool	42.9
Lung ca. HOP-62	7.0	Cerebral Cortex Pool	100.0
Lung ca. NCI-H522	2.9	Brain (Substantia nigra) Pool	76.3
Liver	0.1	Brain (Thalamus) Pool	63.7
Fetal Liver	1.3	Brain (whole)	56.6
Liver ca. HepG2	1.4	Spinal Cord Pool	9.3
Kidney Pool	26.2	Adrenal Gland	16.2
Fetal Kidney	3.5	Pituitary gland Pool	16.4
Renal ca. 786-0	26.4	Salivary Gland	13.4
Renal ca. Q-S		Pancreas Pool	

Table SD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3317, Run 164683049	Tissue Name	Rel. Exp.(%) Ag3317, Run 164683049
Secondary Th1 act	21.6	HUVEC IL-1beta	3.8
Secondary Th2 act	23.2	HUVEC IFN gamma	12.5
Secondary Tr1 act	22.8	HUVEC TNF alpha + IFN gamma	2.9
Secondary Th1 rest	12.7	HUVEC TNF alpha + IL4	9.0
Secondary Th2 rest	9.3	HUVEC IL-11	4.0
Secondary Tr1 rest	33.7	Lung Microvascular EC none	24.3
Primary Th1 act	44.1	Lung Microvascular EC TNFalpha + IL-1beta	11.3
Primary Th2 act	49.3	Microvascular Dermal EC none	41.5
Primary Tr1 act	74.2	Microvascular Dermal EC TNFalpha + IL-1beta	17.2
Primary Th1 rest	38.2	Bronchial epithelium TNFalpha + IL1beta	31.2
Primary Th2 rest	44.4	Small airway epithelium none	8.0
Primary Tr1 rest	50.0	Small airway epithelium TNFalpha + IL-1beta	11.1
CD45RA CD4 lymphocyte act	41.2	Coronary artery SMC rest	20.6
CD45RO CD4 lymphocyte act	25.0	Coronary artery SMC TNFalpha + IL-1beta	19.6
CD8 lymphocyte act	17.8	Astrocytes rest	14.7
Secondary CD8 lymphocyte rest	21.8	Astrocytes TNFalpha + IL-1beta	11.0
Secondary CD8 lymphocyte act	7.4	KU-812 (Basophil) rest	2.1
CD4 lymphocyte none	21.8	KU-812 (Basophil) PMA/ionomycin	12.9
2ry Th1/Th2/Tr1_anti- CD95 CH11	5.8	CCD1106 (Keratinocytes) none	30.6
LAK cells rest	51.1	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	23.7
LAK cells IL-2	7.0	Liver cirrhosis	0.8
gamma			
LAK cells IL-2+ IL-18	28.7	NCI-H292 IL-4	43.5

LAK cells PMA/ionomycin	20.6	NCI-H292 IL-9	36.3
NK Cells IL-2 rest	13.5	NCI-H292 IL-13	35.6
Two Way MLR 3 day	33.0	NCI-H292 IFN gamma	24.3
Two Way MLR 5 day	9.6	HPAEC none	22.8
Two Way MLR 7 day	10.0	HPAEC TNF alpha + IL-1 beta	8.3
PBMC rest	12.0	Lung fibroblast none	11.8
PBMC PWM	24.7	Lung fibroblast TNF alpha + IL-1 beta	1.2
PBMC PHA-L	32.5	Lung fibroblast IL-4	19.2
Ramos (B cell) none	1.5	Lung fibroblast IL-9	12.1
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	14.8
B lymphocytes PWM	41.2	Lung fibroblast IFN gamma	17.2
B lymphocytes CD40L and IL-4	14.5	Dermal fibroblast CCD1070 rest	100.0
EOL-1 dbcAMP	20.0	Dermal fibroblast CCD1070 TNF alpha	57.8
EOL-1 dbcAMP PMA/ionomycin	60.3	Dermal fibroblast CCD1070 IL-1 beta	14.2
Dendritic cells none	55.5	Dermal fibroblast IFN gamma	24.1
Dendritic cells LPS	26.1	Dermal fibroblast IL-4	39.0
Dendritic cells anti- CD40	74.7	IBD Colitis 2	1.6
Monocytes rest	48.0	IBD Crohn's	2.7
Monocytes LPS	15.4	Colon	19.1
Macrophages rest	98.6	Lung	14.4
Macrophages LPS	5.6	Thymus	10.5
HUVEC none	27.9	Kidney	100.0
HUVEC starved	27.0		

CNS_neurodegeneration_v1.0 Summary: Ag3317 - This panel does not show differential expression of this gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.4 for discussion of utility of this gene in the central nervous system.

throughout the CNS, including in amygdala, substantia nigra, thalamus, cerebellum, and

cerebral cortex. Highest expression is observed in the cerebral cortex (CT=29.0). This gene encodes a calmodulin-dependent protein kinase IV homolog, which is known to play a role in Ca^{2+} signaling in the CNS that controls neuronal growth, differentiation, and plasticity. Mice deficient in calmodulin-dependent protein kinase IV were found to have cerebellar defects. Therefore, this gene may play a role in central nervous system disorders such as Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

Based on expression in this panel, this gene may be also be involved in gastric, pancreatic, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

References:

1. Okuno S, Kitani T, Fujisawa H. Evidence for the existence of Ca^{2+} /calmodulin-dependent protein kinase IV kinase isoforms in rat brain. *J Biochem (Tokyo)* 1996 Jun;119(6):1176-81.
2. Ribar TJ, Rodriguiz RM, Khiroug L, Wetsel WC, Augustine GJ, Means AR. Cerebellar defects in Ca^{2+} /calmodulin kinase IV-deficient mice. *J Neurosci* 2000 Nov 15;20(22):RC107.

Panel 4D Summary: Ag3317 - This gene was found to have low expression across almost all the samples on this panel, with the highest level of expression seen in kidney and resting dermal fibroblasts (CTs=32). Expression of Ca^{2+} /calmodulin-dependent kinase type IV in thymocytes has been found in mice, where it plays a role in Ca^{2+} -dependent gene transcription.

1. Raman V, Blaeser F, Ho N, Engle DL, Williams CB, Chatila TA. Requirement for Ca²⁺/calmodulin-dependent kinase type IV/Gr in setting the thymocyte selection threshold. J Immunol 2001 Dec 1;167(11):6270-8.

T. CG57709-01: Novel mitochondrial protein

Expression of gene CG57709-01 was assessed using the primer-probe set Ag3323, described in Table TA. Results of the RTQ-PCR runs are shown in Tables TB, TC and TD.

Table TA. Probe Name Ag3323

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-atgtgcagaggatacgcacg-3'	20	589	450
Probe	TET-5'-tgcaaacacaggaacacaaqqaaggg-3'- TAMRA	26	626	451
Reverse	5'-tggttctggcattctagacg-3'	20	665	452

Table TB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3323, Run 210144152	Tissue Name	Rel. Exp.(%) Ag3323, Run 210144152
AD 1 Hippo	22.5	Control (Path) 3 Temporal Ctx	5.2
AD 2 Hippo	29.5	Control (Path) 4 Temporal Ctx	32.5
AD 3 Hippo	6.9	AD 1 Occipital Ctx	18.6
AD 4 Hippo	7.4	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	82.4	AD 3 Occipital Ctx	7.6
AD 6 Hippo	66.4	AD 4 Occipital Ctx	17.8
Control 2 Hippo	27.5	AD 5 Occipital Ctx	30.8
Control 4 Hippo	11.9	AD 6 Occipital Ctx	48.6
Control (Path) 3 Hippo	8.4	Control 1 Occipital Ctx	4.0
AD 1 Temporal Ctx	18.6	Control 2 Occipital Ctx	58.2
AD 2 Temporal Ctx	30.6	Control 3 Occipital Ctx	14.2

AD 4 Temporal Ctx

Control (Path)
Occipital Ctx

AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	12.6
AD 5 Sup Temporal Ctx	42.6	Control (Path) 3 Occipital Ctx	2.4
AD 6 Inf Temporal Ctx	48.6	Control (Path) 4 Occipital Ctx	14.6
AD 6 Sup Temporal Ctx	42.0	Control 1 Parietal Ctx	6.5
Control 1 Temporal Ctx	6.3	Control 2 Parietal Ctx	48.0
Control 2 Temporal Ctx	39.0	Control 3 Parietal Ctx	19.6
Control 3 Temporal Ctx	13.1	Control (Path) 1 Parietal Ctx	61.1
Control 4 Temporal Ctx	8.9	Control (Path) 2 Parietal Ctx	19.3
Control (Path) 1 Temporal Ctx	53.6	Control (Path) 3 Parietal Ctx	3.8
Control (Path) 2 Temporal Ctx	34.2	Control (Path) 4 Parietal Ctx	42.6

Table TC. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3323, Run 165678151	Tissue Name	Rel. Exp.(%) Ag3323, Run 165678151
Liver adenocarcinoma	25.0	Kidney (fetal)	6.5
Pancreas	12.8	Renal ca. 786-0	14.3
Pancreatic ca. CAPAN 2	24.5	Renal ca. A498	34.2
Adrenal gland	12.2	Renal ca. RXF 393	14.2
Thyroid	6.9	Renal ca. ACHN	12.9
Salivary gland	14.0	Renal ca. UO-31	48.6
Pituitary gland	10.1	Renal ca. TK-10	7.2
Brain (fetal)	13.7	Liver	20.2
Brain (whole)	29.7	Liver (fetal)	22.1
Brain (amygdala)	21.3	Liver ca. (hepatoblast) HepG2	21.3
Brain (cerebellum)	24.7	Lung	6.7
Brain (hippocampus)	25.7	Lung (fetal)	14.8
Brain (substantia nigra)	20.0	Lung ca. (small cell)	39.8
Cerebral Cortex	33.0	Lung ca. (s cell var)	42.3

		SHP-77	
Spinal cord	16.5	Lung ca. (large cell)NCI-H460	25.7
glio/astro U87-MG	8.9	Lung ca. (non-sm. cell) A549	12.0
glio/astro U-118-MG	100.0	Lung ca. (non-s.cell) NCI-H23	9.1
astrocytoma SW1783	14.6	Lung ca. (non-s.cell) HOP-62	9.5
neuro*; met SK-N-AS	43.2	Lung ca. (non-s.cl) NCI-H522	10.7
astrocytoma SF-539	13.9	Lung ca. (squam.) SW 900	12.4
astrocytoma SNB-75	29.7	Lung ca. (squam.) NCI-H596	59.0
glioma SNB-19	13.5	Mammary gland	10.6
glioma U251	43.8	Breast ca.* (pl.ef) MCF-7	46.3
glioma SF-295	17.7	Breast ca.* (pl.ef) MDA-MB-231	31.6
Heart (fetal)	22.7	Breast ca.* (pl.ef) T47D	15.1
Heart	14.5	Breast ca. BT-549	54.0
Skeletal muscle (fetal)	6.8	Breast ca. MDA-N	11.5
Skeletal muscle	55.5	Ovary	8.7
Bone marrow	10.7	Ovarian ca. OVCAR-3	26.2
Thymus	5.5	Ovarian ca. OVCAR-4	21.6
Spleen	13.3	Ovarian ca. OVCAR-5	20.9
Lymph node	24.8	Ovarian ca. OVCAR-8	12.6
Colorectal	8.8	Ovarian ca. IGROV-1	4.4
Stomach	15.1	Ovarian ca.* (ascites) SK-OV-3	23.5
Small intestine	28.3	Uterus	14.3
Colon ca. SW480	27.5	Placenta	6.9
Colon ca.* SW620(SW480 met)	17.6	Prostate	9.5
Colon ca. HCT-116	12.7	Testis	7.6
Colon ca. CaCo-2	12.7	Melanoma	7.6

		Hs688(A).T	
Colon ca. tissue(ODO3866)	22.5	Melanoma* (met) Hs688(B).T	6.6
Colon ca. HCC-2998	25.2	Melanoma UACC-62	19.6
Gastric ca.* (liver met) NCI-N87	29.5	Melanoma M14	39.2
Bladder	6.1	Melanoma LOX IMVI	13.4
Trachea	13.2	Melanoma* (met) SK-MEL-5	21.2
Kidney	15.6	Adipose	6.5

Table TD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3323, Run 165296416	Tissue Name	Rel. Exp.(%) Ag3323, Run 165296416
Secondary Th1 act	32.3	HUVEC IL-1beta	3.8
Secondary Th2 act	22.8	HUVEC IFN gamma	12.0
Secondary Tr1 act	29.9	HUVEC TNF alpha + IFN gamma	8.1
Secondary Th1 rest	3.8	HUVEC TNF alpha + IL4	11.1
Secondary Th2 rest	4.3	HUVEC IL-11	8.4
Secondary Tr1 rest	6.0	Lung Microvascular EC none	7.6
Primary Th1 act	33.0	Lung Microvascular EC TNFalpha + IL-1beta	6.9
Primary Th2 act	25.0	Microvascular Dermal EC none	14.7
Primary Tr1 act	40.1	Microvascular Dermal EC TNFalpha + IL-1beta	7.6
Primary Th1 rest	17.8	Bronchial epithelium TNFalpha + IL1beta	17.3
Primary Th2 rest	11.6	Small airway epithelium none	6.6
Primary Tr1 rest	15.0	Small airway epithelium TNFalpha + IL-1beta	18.4
CD45RA CD4 lymphocyte act	15.0	Coronary artery SMC rest	9.9
CD45RO CD4 lymphocyte act	24.7	Coronary artery SMC TNFalpha + IL-1beta	6.5
lymphocyte rest		IL-1beta	
Secondary CD8	12.9	KU-812 (Basophil) rest	14.0

lymphocyte act			
CD4 lymphocyte none	2.9	KU-812 (Basophil) PMA/ionomycin	22.1
2ry Th1/Th2/Tr1_anti- CD95 CH11	5.4	CCD1106 (Keratinocytes) none	16.0
LAK cells rest	7.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	8.1
LAK cells IL-2	17.2	Liver cirrhosis	1.7
LAK cells IL-2+IL-12	15.1	Lupus kidney	1.0
LAK cells IL-2+IFN gamma	27.9	NCI-H292 none	30.1
LAK cells IL-2+ IL-18	17.7	NCI-H292 IL-4	49.0
LAK cells PMA/ionomycin	1.9	NCI-H292 IL-9	33.2
NK Cells IL-2 rest	8.4	NCI-H292 IL-13	26.2
Two Way MLR 3 day	9.9	NCI-H292 IFN gamma	26.6
Two Way MLR 5 day	18.4	HPAEC none	11.7
Two Way MLR 7 day	8.9	HPAEC TNF alpha + IL-1 beta	7.5
PBMC rest	3.8	Lung fibroblast none	8.0
PBMC PWM	50.3	Lung fibroblast TNF alpha + IL-1 beta	5.5
PBMC PHA-L	29.3	Lung fibroblast IL-4	19.1
Ramos (B cell) none	33.9	Lung fibroblast IL-9	15.3
Ramos (B cell) ionomycin	83.5	Lung fibroblast IL-13	11.4
B lymphocytes PWM	100.0	Lung fibroblast IFN gamma	16.5
B lymphocytes CD40L and IL-4	22.4	Dermal fibroblast CCD1070 rest	28.9
EOL-1 dbcAMP	10.5	Dermal fibroblast CCD1070 TNF alpha	31.2
EOL-1 dbcAMP PMA/ionomycin	3.7	Dermal fibroblast CCD1070 IL-1 beta	11.3
Dendritic cells none	9.9	Dermal fibroblast IFN gamma	5.2
Dendritic cells LPS	6.3	Dermal fibroblast IL-4	12.3
Dendritic cells anti- CD40	7.3	IBD Colitis 2	0.7
Monocytes rest	7.0	IBD Crohn's	1.0
Macrophages LPS			
HUVEC none	11.9	Kidney	12.3

HUVEC starved	24.8		
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CNS_neurodegeneration_v1.0 Summary: Ag3323 This panel does not show differential expression of the CG57709-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

Panel 1.3D Summary: Ag3323 - This gene is expressed at moderate levels in all samples on this panel, with highest expression in a brain cancer cell line. Expression is also seen in all the cancer cell lines on this panel. Thus, expression of this gene could be used to differentiate between this brain cancer cell line sample and other samples on this panel and as a marker for brain cancer.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

This molecule is also expressed at moderate to low levels in the CNS and may be a small molecule target for the treatment of neurologic diseases such as Alzheimer's disease, Parkinson's disease, epilepsy, schizophrenia, stroke and multiple sclerosis.

Panel 4D Summary: Ag3323 - This gene is expressed at high to moderate levels in all samples on this panel, with highest expression in B lymphocytes stimulated with pokeweed mitogen (CT=24.5). In addition, this gene is expressed at higher levels in ionomycin-activated Ramos B lymphocytes. The high levels of expression in activated B lymphocytes suggests that therapies that antagonize the function of this gene product may reduce or eliminate the symptoms in patients with autoimmune and inflammatory diseases in which B cells play a part in the initiation or progression of the disease process, such as lupus erythematosus, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, or psoriasis.

CG57709-01 HYDROXYMETHYLGLUTARATE HYDROXYMETHYLGLUTARATE HYDROXYMETHYLGLUTARATE
(GLYOXALASE II)

Expression of gene CG57700-01 was assessed using the primer-probe set Ag3311, described in Table UA. Results of the RTQ-PCR runs are shown in Table UB.

Table UA. Probe Name Ag3311

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-acgcttagcaacctggagtt-3'	20	536	453
Probe	TET-5'-accacgtgagagccaagctgtcct-3'- TAMRA	24	582	454
Reverse	5'-gtcctcctcctcctcctccttctg-3'	21	611	456

Table UB. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3311, Run 164682845	Tissue Name	Rel. Exp.(%) Ag3311, Run 164682845
Secondary Th1 act	10.2	HUVEC IL-1beta	0.0
Secondary Th2 act	3.8	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	1.6	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	5.1
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4	0.0	Coronary artery SMC	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0

Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	4.2
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	2.7
LAK cells IL-2	0.0	Liver cirrhosis	0.0
LAK cells IL-2+IL-12	0.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	4.5	NCI-H292 IFN gamma	1.9
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	3.7	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	14.1
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	4.3
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	1.6	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	2.1	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	3.0
Dendritic cells anti-CD40	2.5	IBD Colitis 2	0.0
Macrophages rest	0.0	Thymus	0.0
Macrophages LPS	0.0	Thymus	0.0

HUVEC none	0.0	Kidney	2.4
HUVEC starved	0.0		

AI_comprehensive_panel_v1.0 Summary: Ag3311 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

CNS_neurodegeneration_v1.0 Summary: Ag3311 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3311 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3311 - Significant expression of this gene is seen only in colon (CT=33.9). Therefore, expression of this gene can be used to distinguish between this sample and the others on the panel and between healthy and inflamed bowel. Since expression is not detectable in samples derived from Crohn's and colitis patients, therapeutic modulation of the expression or function of this gene may be useful in the treatment of inflammatory bowel disease.

V. CG58553-01: vasopressin receptor

Expression of gene CG58553-01 was assessed using the primer-probe set Ag3372, described in Table VA. Results of the RTQ-PCR runs are shown in Tables VB and VC.

Table VA. Probe Name Ag3372

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cggatctggtcacacaca 3'	19	1983	457
Probe	TET-5'-ccacccacaacctccaaggaact-3'- TAMRA	24	2017	458
Reverse	5'-agcctcagaaggctcgagatg-3'	20	2041	459

Table VB. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3372, Run 165524269	Tissue Name	Rel. Exp.(%) Ag3372, Run 165524269
Pancreatic ca. CAPAN	0.0	Renal ca. A498	0.1

2			
Adrenal gland	0.0	Renal ca. RXF 393	0.0
Thyroid	0.1	Renal ca. ACHN	0.0
Salivary gland	0.1	Renal ca. UO-31	0.0
Pituitary gland	0.2	Renal ca. TK-10	0.0
Brain (fetal)	0.0	Liver	2.1
Brain (whole)	0.3	Liver (fetal)	0.0
Brain (amygdala)	0.0	Liver ca. (hepatoblast) HepG2	0.2
Brain (cerebellum)	0.1	Lung	2.4
Brain (hippocampus)	0.5	Lung (fetal)	0.2
Brain (substantia nigra)	0.2	Lung ca. (small cell) LX-1	0.0
Brain (thalamus)	0.0	Lung ca. (small cell) NCI-H69	0.0
Cerebral Cortex	0.0	Lung ca. (s.cell var.) SHP-77	0.1
Spinal cord	1.0	Lung ca. (large cell)NCI-H460	0.0
glio/astro U87-MG	0.0	Lung ca. (non-sm. cell) A549	0.1
glio/astro U-118-MG	0.0	Lung ca. (non-s.cell) NCI-H23	0.6
astrocytoma SW1783	0.0	Lung ca. (non-s.cell) HOP-62	0.1
neuro*; met SK-N-AS	0.0	Lung ca. (non-s.cl) NCI-H522	0.0
astrocytoma SF-539	0.0	Lung ca. (squam.) SW 900	0.0
astrocytoma SNB-75	0.1	Lung ca. (squam.) NCI-H596	0.0
glioma SNB-19	0.4	Mammary gland	0.7
glioma U251	0.2	Breast ca.* (pl.ef) MCF-7	0.0
glioma SF-295	0.0	Breast ca.* (pl.ef) MDA-MB-231	0.0
Heart (fetal)	0.0	Breast ca.* (pl.ef) T47D	0.1
Heart	0.0	Breast ca. BT-549	0.0
Skeletal muscle (fetal)	0.0	Breast ca. MDA-N	0.0
Thymus	1.0	Ovarian ca. OVCAR-	0.0

		4	
Spleen	2.8	Ovarian ca. OVCAR-5	0.2
Lymph node	5.5	Ovarian ca. OVCAR-8	0.2
Colorectal	0.2	Ovarian ca. IGROV-1	0.0
Stomach	1.2	Ovarian ca.* (ascites) SK-OV-3	0.0
Small intestine	100.0	Uterus	0.0
Colon ca. SW480	0.0	Placenta	0.8
Colon ca.* SW620(SW480 met)	0.0	Prostate	0.1
Colon ca. HT29	0.0	Prostate ca.* (bone met)PC-3	0.0
Colon ca. HCT-116	0.0	Testis	1.4
Colon ca. CaCo-2	0.3	Melanoma Hs688(A).T	0.0
Colon ca. tissue(ODO3866)	0.7	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	3.8	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	1.0	Melanoma M14	0.2
Bladder	0.0	Melanoma LOX IMVI	0.2
Trachea	0.1	Melanoma* (met) SK-MEL-5	0.4
Kidney	0.6	Adipose	1.3

Table VC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3372, Run 165296616	Tissue Name	Rel. Exp.(%) Ag3372, Run 165296616
Secondary Th1 act	1.4	HUVEC IL-1beta	0.0
Secondary Th2 act	1.4	HUVEC IFN gamma	0.0
Secondary Tr1 act	2.9	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	5.4	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	6.4	HUVEC IL-11	0.0

Primary T cell act

 HUVEC TNF alpha + IL-1beta
 HUVEC TNF alpha + IL-1beta

Primary Th2 act	18.9	Microvascular Dermal EC none	0.0
Primary Tr1 act	27.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	27.5	Bronchial epithelium TNFalpha + IL1beta	0.1
Primary Th2 rest	13.6	Small airway epithelium none	0.0
Primary Tr1 rest	32.8	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	3.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	8.5	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	5.8	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	3.1	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	2.9	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	4.7	KU-812 (Basophil) PMA/ionomycin	0.1
2ry Th1/Th2/Tr1_anti-CD95 CH11	7.5	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	1.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	5.8	Liver cirrhosis	1.5
LAK cells IL-2+IL-12	2.3	Lupus kidney	0.6
LAK cells IL-2+IFN gamma	5.5	NCI-H292 none	2.5
LAK cells IL-2+ IL-18	5.5	NCI-H292 IL-4	1.8
LAK cells PMA/ionomycin	2.7	NCI-H292 IL-9	5.9
NK Cells IL-2 rest	6.0	NCI-H292 IL-13	2.3
Two Way MLR 3 day	2.1	NCI-H292 IFN gamma	3.0
Two Way MLR 5 day	0.9	HPAEC none	0.0
Two Way MLR 7 day	1.8	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	1.5	Lung fibroblast none	0.0
PBMC PWM	5.6	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PMA + I	0.0	Lung fibroblast IL-4	0.0
Naïve CD4 cells PMA/ionomycin	0.0	Lung fibroblast IL-4	0.0
B lymphocytes PWM	2.2	Lung fibroblast IFN	0.0

		gamma	
B lymphocytes CD40L and IL-4	3.7	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	1.0	Dermal fibroblast CCD1070 TNF alpha	5.2
EOL-1 dbcAMP PMA/ionomycin	0.4	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.2	Dermal fibroblast IFN gamma	0.1
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti-CD40	0.0	IBD Colitis 2	0.4
Monocytes rest	0.3	IBD Crohn's	8.4
Monocytes LPS	0.2	Colon	100.0
Macrophages rest	0.7	Lung	0.9
Macrophages LPS	0.0	Thymus	8.1
HUVEC none	0.0	Kidney	6.8
HUVEC starved	0.0		

Panel 1.3D Summary: Ag3372 Highest expression of the CG58553-01 gene is seen in the small intestine sample (CT=26.8). This gene encodes a novel vasopressin gene that plays a role in regulating electrolyte transport in the colon. Therefore, regulation of the transcript or the protein it encodes could be important in maintaining normal cellular homeostasis and in the treatment of Crohn's disease and ulcerative colitis.

Among tissues with metabolic function, this gene is expressed in liver and adipose. Thus, this gene product may be involved in disorders that affect these tissues, such as obesity and type II diabetes.

Low, but significant expression is also seen in the hippocampus. The hippocampus is critical for learning and memory. Thus, this gene product may have utility treating CNS disorders involving memory deficits, including Alzheimer's disease and aging.

References:

1. Sato Y, Hanai H, Nogaki A, Hirasawa K, Kaneko E, Hayashi H, Suzuki Y. Role of the vasopressin V1b receptor in regulating the epithelial functions of the avian mid-intestine.

Panel 4D Summary: Ag3372 In agreement with the results seen in panel 1.4, the highest level of expression of this gene is in the colon sample (CT=27.5). Interestingly, the expression is significantly lower in the IBD colitis 2 (CT>35) and IBD Crohn's (CT=30.9) samples. Therefore, alterations in the expression of this gene may be used in the treatment of Crohn's disease and ulcerative colitis.

In addition, the expression of the CG58553-01 gene in several preparations of T lymphocytes suggests that small molecule antagonists, therapeutic antibodies specific for this molecule, or the extracellular domain of this protein, may be useful to reduce or eliminate the symptoms of Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, lupus erythematosus, or psoriasis.

W. CG58626-01: Phospholipase

Expression of gene CG58626-01 was assessed using the primer-probe set Ag3386, described in Table WA. Results of the RTQ-PCR runs are shown in Tables WB, WC and WD.

Table WA. Probe Name Ag3386

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - agtggcggtcaaaacttactct - 3'	22	1386	460
Probe	TET-5' - tggagacactgttgattccattactcctg-3' - TAMRA	29	1411	461
Reverse	5' - ctgctgttcagcatatccctta - 3'	22	1455	462

Table WB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3386, Run 210154893	Tissue Name	Rel. Exp.(%) Ag3386, Run 210154893
AD 1 Hippo	6.4	Control (Path) 3 Temporal Ctx	4.2
AD 2 Hippo	21.5	Control (Path) 4 Temporal Ctx	25.0
AD 3 Hippo	5.0	AD 1 Occipital Ctx	14.4
		AD 2 Occipital Ctx	
AD 6 Hippo	21.1	AD 4 Occipital Ctx	28.7
Control 2 Hippo	26.4	AD 5 Occipital Ctx	28.7

Control 4 Hippo	4.5	AD 6 Occipital Ctx	52.5
Control (Path) 3 Hippo	4.0	Control 1 Occipital Ctx	2.4
AD 1 Temporal Ctx	13.5	Control 2 Occipital Ctx	56.3
AD 2 Temporal Ctx	24.5	Control 3 Occipital Ctx	11.0
AD 3 Temporal Ctx	3.8	Control 4 Occipital Ctx	4.3
AD 4 Temporal Ctx	18.9	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	95.9	Control (Path) 2 Occipital Ctx	8.8
AD 5 Sup Temporal Ctx	37.6	Control (Path) 3 Occipital Ctx	1.7
AD 6 Inf Temporal Ctx	52.5	Control (Path) 4 Occipital Ctx	12.3
AD 6 Sup Temporal Ctx	63.7	Control 1 Parietal Ctx	5.4
Control 1 Temporal Ctx	4.9	Control 2 Parietal Ctx	39.5
Control 2 Temporal Ctx	38.4	Control 3 Parietal Ctx	11.3
Control 3 Temporal Ctx	12.2	Control (Path) 1 Parietal Ctx	77.4
Control 4 Temporal Ctx	5.0	Control (Path) 2 Parietal Ctx	20.7
Control (Path) 1 Temporal Ctx	76.8	Control (Path) 3 Parietal Ctx	2.7
Control (Path) 2 Temporal Ctx	37.6	Control (Path) 4 Parietal Ctx	45.4

Table WC. General screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3386, Run 217043839	Tissue Name	Rel. Exp.(%) Ag3386, Run 217043839
Adipose	12.2	Renal ca. TK-10	10.7
Melanoma* Hs688(A).T	26.4	Bladder	18.4
Melanoma* Hs688(B).T	30.4	Gastric ca. (liver met.) NCI-N87	26.6
COXIMV1			
Melanoma* SK-	22.7	Colon ca. SW480	40.9

MEL-5			
Squamous cell carcinoma SCC-4	11.2	Colon ca.* (SW480 met) SW620	20.4
Testis Pool	47.0	Colon ca. HT29	5.2
Prostate ca.* (bone met) PC-3	80.1	Colon ca. HCT-116	100.0
Prostate Pool	7.1	Colon ca. CaCo-2	13.8
Placenta	3.2	Colon cancer tissue	13.6
Uterus Pool	6.4	Colon ca. SW1116	10.2
Ovarian ca. OVCAR-3	22.8	Colon ca. Colo-205	1.8
Ovarian ca. SK-OV-3	94.0	Colon ca. SW-48	2.4
Ovarian ca. OVCAR-4	4.7	Colon Pool	27.7
Ovarian ca. OVCAR-5	29.3	Small Intestine Pool	14.6
Ovarian ca. IGROV-1	12.7	Stomach Pool	12.2
Ovarian ca. OVCAR-8	11.1	Bone Marrow Pool	6.9
Ovary	11.6	Fetal Heart	8.1
Breast ca. MCF-7	36.9	Heart Pool	6.3
Breast ca. MDA-MB-231	39.5	Lymph Node Pool	13.9
Breast ca. BT 549	28.5	Fetal Skeletal Muscle	3.6
Breast ca. T47D	52.9	Skeletal Muscle Pool	6.7
Breast ca. MDA-N	11.3	Spleen Pool	17.1
Breast Pool	28.1	Thymus Pool	26.1
Trachea	11.0	CNS cancer (glio/astro) U87-MG	33.2
Lung	6.0	CNS cancer (glio/astro) U-118-MG	44.1
Fetal Lung	39.2	CNS cancer (neuro;met) SK-N-AS	44.4
Lung ca. NCI-N417	6.3	CNS cancer (astro) SF-539	10.4
Lung ca. LX-1	33.9	CNS cancer (astro) SNB-75	27.7
Lung ca. NCI-H146	14.3	CNS cancer (glio) SNB-19	10.2
Lung ca. A549	25.5	Bram (Amygdala) Pool	23.2

Lung ca. NCI-H526	5.8	Brain (cerebellum)	19.8
Lung ca. NCI-H23	30.1	Brain (fetal)	35.6
Lung ca. NCI-H460	20.2	Brain (Hippocampus) Pool	25.2
Lung ca. HOP-62	11.9	Cerebral Cortex Pool	39.2
Lung ca. NCI-H522	20.7	Brain (Substantia nigra) Pool	23.0
Liver	0.7	Brain (Thalamus) Pool	45.7
Fetal Liver	29.5	Brain (whole)	24.0
Liver ca. HepG2	10.1	Spinal Cord Pool	22.5
Kidney Pool	21.3	Adrenal Gland	8.5
Fetal Kidney	19.5	Pituitary gland Pool	7.0
Renal ca. 786-0	15.9	Salivary Gland	1.9
Renal ca. A498	3.5	Thyroid (female)	3.2
Renal ca. ACHN	8.0	Pancreatic ca. CAPAN2	3.7
Renal ca. UO-31	12.2	Pancreas Pool	18.2

Table WD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3386, Run 165296474	Tissue Name	Rel. Exp.(%) Ag3386, Run 165296474
Secondary Th1 act	30.4	HUVEC IL-1beta	2.0
Secondary Th2 act	35.6	HUVEC IFN gamma	3.3
Secondary Tr1 act	27.9	HUVEC TNF alpha + IFN gamma	3.8
Secondary Th1 rest	8.9	HUVEC TNF alpha + IL4	3.3
Secondary Th2 rest	8.0	HUVEC IL-11	1.5
Secondary Tr1 rest	11.3	Lung Microvascular EC none	5.5
Primary Th1 act	57.4	Lung Microvascular EC TNFalpha + IL-1beta	4.8
Primary Th2 act	36.9	Microvascular Dermal EC none	3.7
Primary Tr1 act	51.1	Microvascular Dermal EC TNFalpha + IL-1beta	3.3
Primary Th1 rest	54.0	Bronchial epithelium TNFalpha + IL1beta	5.5
Primary Th2 rest	18.8	Small airway epithelium none	2.1
CD45RA CD4 lymphocyte act	12.4	Coronary artery SMC rest	4.6

CD45RO CD4 lymphocyte act	33.9	Coronary artery SMC TNFalpha + IL-1beta	2.4
CD8 lymphocyte act	29.3	Astrocytes rest	3.0
Secondary CD8 lymphocyte rest	26.1	Astrocytes TNFalpha + IL-1beta	3.0
Secondary CD8 lymphocyte act	20.7	KU-812 (Basophil) rest	12.1
CD4 lymphocyte none	1.1	KU-812 (Basophil) PMA/ionomycin	27.7
2ry Th1/Th2/Tr1_anti-CD95 CH11	12.8	CCD1106 (Keratinocytes) none	2.7
LAK cells rest	12.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.8
LAK cells IL-2	24.3	Liver cirrhosis	0.3
LAK cells IL-2+IL-12	28.7	Lupus kidney	0.7
LAK cells IL-2+IFN gamma	42.0	NCI-H292 none	8.1
LAK cells IL-2+ IL-18	45.1	NCI-H292 IL-4	9.5
LAK cells PMA/ionomycin	8.8	NCI-H292 IL-9	8.5
NK Cells IL-2 rest	21.8	NCI-H292 IL-13	4.5
Two Way MLR 3 day	18.7	NCI-H292 IFN gamma	3.6
Two Way MLR 5 day	11.0	HPAEC none	2.5
Two Way MLR 7 day	10.9	HPAEC TNF alpha + IL-1 beta	3.0
PBMC rest	4.5	Lung fibroblast none	4.6
PBMC PWM	66.0	Lung fibroblast TNF alpha + IL-1 beta	3.3
PBMC PHA-L	17.9	Lung fibroblast IL-4	12.1
Ramos (B cell) none	26.1	Lung fibroblast IL-9	12.3
Ramos (B cell) ionomycin	100.0	Lung fibroblast IL-13	6.7
B lymphocytes PWM	88.9	Lung fibroblast IFN gamma	16.6
B lymphocytes CD40L and IL-4	49.3	Dermal fibroblast CCD1070 rest	8.2
EOL-1 dbcAMP	13.0	Dermal fibroblast CCD1070 TNF alpha	37.1
EOL-1 dbcAMP PMA/ionomycin	9.5	Dermal fibroblast CCD1070 IL-1 beta	4.4
		Dermal fibroblast IFN	
Dendritic cells anti CD40	4.3	IBD Colitis 2	0.7

Monocytes rest	4.7	IBD Crohn's	0.5
Monocytes LPS	2.6	Colon	3.4
Macrophages rest	8.8	Lung	4.9
Macrophages LPS	2.8	Thymus	4.1
HUVEC none	2.8	Kidney	13.0
HUVEC starved	6.4		

CNS_neurodegeneration_v1.0 Summary: Ag3386 This panel confirms the expression of this gene at moderate to low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3386 This gene is moderately expressed in most of the samples on this panel. Based on expression in this panel, this gene may be involved in gastric, pancreatic, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene is expressed at moderate levels in the CNS. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3386 The CG58626-01 transcript is expressed ubiquitously in this panel. Highest expression of this transcript is seen in activated Ramos cells and activated B cells (CTs=27). The expression of this transcript in activated lymphoid cells when compared to non-activated cells suggests that the CG58626-01 gene may be important for the diagnosis

of activated cells. This gene product might be important for the treatment of autoimmune disease, allergy, and delayed type hypersensitivity.

X. CG57597-01: Hypothetical protein

Expression of gene CG57597-01 was assessed using the primer-probe set Ag3293, described in Table XA.

Table XA. Probe Name Ag3293

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cagaaacctgtgaactctgcat-3'	22	40	463
Probe	TET-5'-atgcaccaccactcctggctaatttt-3'- TAMRA	26	69	464
Reverse	5'-ataaaagggttgagccggatt-3'	21	115	465

CNS_neurodegeneration_v1.0 Summary: Ag3293 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3293 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Panel 4D Summary: Ag3293 - Expression of this gene is low/undetectable (CTs > 35) across all of the samples on this panel (data not shown).

Y. CG57804-01: talin

Expression of gene CG57804-01 was assessed using the primer-probe set Ag3337, described in Table YA. Results of the RTQ-PCR runs are shown in Tables YB, YC and YD.

Table YA. Probe Name Ag3337

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ggatttcaagcccagatacaat-3'	22	781	466
Probe	TET-5'-tggacctcatgtggaacataaacaca-3'- TAMRA	26	804	467
Reverse	5'-ggcaggaattccttcagatc-3'	20	844	468

Tissue Name	Rel. Exp.(%) Ag3337,	Tissue Name	Rel. Exp.(%) Ag3337,
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	Run 210138775		Run 210138775
AD 1 Hippo	6.8	Control (Path) 3 Temporal Ctx	3.6
AD 2 Hippo	25.3	Control (Path) 4 Temporal Ctx	22.4
AD 3 Hippo	3.6	AD 1 Occipital Ctx	5.6
AD 4 Hippo	5.7	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	78.5	AD 3 Occipital Ctx	2.2
AD 6 Hippo	27.5	AD 4 Occipital Ctx	14.7
Control 2 Hippo	27.4	AD 5 Occipital Ctx	44.1
Control 4 Hippo	8.1	AD 6 Occipital Ctx	16.6
Control (Path) 3 Hippo	4.3	Control 1 Occipital Ctx	1.6
AD 1 Temporal Ctx	7.6	Control 2 Occipital Ctx	67.8
AD 2 Temporal Ctx	24.5	Control 3 Occipital Ctx	11.9
AD 3 Temporal Ctx	3.3	Control 4 Occipital Ctx	3.0
AD 4 Temporal Ctx	15.3	Control (Path) 1 Occipital Ctx	89.5
AD 5 Inf Temporal Ctx	89.5	Control (Path) 2 Occipital Ctx	8.2
AD 5 Sup Temporal Ctx	35.8	Control (Path) 3 Occipital Ctx	0.6
AD 6 Inf Temporal Ctx	27.4	Control (Path) 4 Occipital Ctx	10.3
AD 6 Sup Temporal Ctx	32.8	Control 1 Parietal Ctx	3.6
Control 1 Temporal Ctx	3.4	Control 2 Parietal Ctx	23.7
Control 2 Temporal Ctx	47.6	Control 3 Parietal Ctx	14.1
Control 3 Temporal Ctx	12.4	Control (Path) 1 Parietal Ctx	100.0
Control 3 Temporal Ctx	5.8	Control (Path) 2 Parietal Ctx	21.9
Control (Path) 1 Temporal Ctx	64.2	Control (Path) 3 Parietal Ctx	2.0
Control (Path) 2		Control (Path) 4	

Table 13: General Screening Data (continued)

Tissue Name	Rel. Exp.(%) Ag3337, Run 215773748	Tissue Name	Rel. Exp.(%) Ag3337, Run 215773748
Adipose	20.2	Renal ca. TK-10	22.1
Melanoma* Hs688(A).T	58.6	Bladder	14.2
Melanoma* Hs688(B).T	22.8	Gastric ca. (liver met.) NCI-N87	16.2
Melanoma* M14	5.7	Gastric ca. KATO III	100.0
Melanoma* LOXIMVI	5.5	Colon ca. SW-948	16.3
Melanoma* SK- MEL-5	3.4	Colon ca. SW480	4.2
Squamous cell carcinoma SCC-4	4.4	Colon ca. * (SW480 met) SW620	2.6
Testis Pool	5.1	Colon ca. HT29	0.7
Prostate ca. * (bone met) PC-3	6.4	Colon ca. HCT-116	7.6
Prostate Pool	3.4	Colon ca. CaCo-2	81.8
Placenta	1.6	Colon cancer tissue	1.7
Uterus Pool	2.1	Colon ca. SW1116	1.6
Ovarian ca. OVCAR-3	8.9	Colon ca. Colo-205	0.1
Ovarian ca. SK-OV- 3	32.1	Colon ca. SW-48	3.2
Ovarian ca. OVCAR-4	7.2	Colon Pool	8.0
Ovarian ca. OVCAR-5	21.0	Small Intestine Pool	7.9
Ovarian ca. IGROV- 1	23.5	Stomach Pool	5.7
Ovarian ca. OVCAR-8	5.4	Bone Marrow Pool	3.8
Ovary	11.7	Fetal Heart	24.8
Breast ca. MCF-7	5.1	Heart Pool	10.2
Breast ca. MDA- MB-231	19.5	Lymph Node Pool	10.6
Breast ca. BT 549	11.7	Fetal Skeletal Muscle	30.1
Breast ca. T47D	30.8	Skeletal Muscle Pool	24.8
Breast ca. MDA-N	5.0	Spleen Pool	2.9
Breast Pool	6.9	Thymus Pool	0.0

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Fetal Lung	10.8	CNS cancer (neuro;met) SK-N-AS	23.5
Lung ca. NCI-N417	0.8	CNS cancer (astro) SF-539	21.5
Lung ca. LX-1	1.7	CNS cancer (astro) SNB-75	40.3
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	27.7
Lung ca. SHP-77	11.9	CNS cancer (glio) SF-295	38.2
Lung ca. A549	13.6	Brain (Amygdala) Pool	28.7
Lung ca. NCI-H526	7.6	Brain (cerebellum)	38.7
Lung ca. NCI-H23	10.2	Brain (fetal)	58.6
Lung ca. NCI-H460	5.1	Brain (Hippocampus) Pool	25.7
Lung ca. HOP-62	3.8	Cerebral Cortex Pool	59.0
Lung ca. NCI-H522	10.1	Brain (Substantia nigra) Pool	39.2
Liver	0.3	Brain (Thalamus) Pool	51.4
Fetal Liver	15.3	Brain (whole)	58.2
Liver ca. HepG2	53.2	Spinal Cord Pool	18.6
Kidney Pool	18.4	Adrenal Gland	11.1
Fetal Kidney	11.4	Pituitary gland Pool	4.7
Renal ca. 786-0	31.0	Salivary Gland	14.0
Renal ca. A498	0.7	Thyroid (female)	4.9
Renal ca. ACHN	20.3	Pancreatic ca. CAPAN2	7.5
Renal ca. UO-31	8.1	Pancreas Pool	9.4

Table YD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3337, Run 165725932	Tissue Name	Rel. Exp.(%) Ag3337, Run 165725932
Secondary Th1 act	0.0	HUVEC IL-1beta	0.7
Secondary Th2 act	0.0	HUVEC IFN gamma	3.9
Secondary Tr1 act	0.4	HUVEC TNF alpha + IFN gamma	0.3
Secondary Th1 rest	0.4	HUVEC TNF alpha + IL4	0.6
Secondary Th2 rest	0.0	HUVEC IL-11	0.3

Primary Th2 act	1.3	Microvascular Dermal EC	16.4
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		none	
Primary Tr1 act	0.6	Microvascular Dermal EC TNFalpha + IL-1beta	9.8
Primary Th1 rest	1.3	Bronchial epithelium TNFalpha + IL1beta	1.2
Primary Th2 rest	0.6	Small airway epithelium none	1.3
Primary Tr1 rest	0.3	Small airway epithelium TNFalpha + IL-1beta	2.1
CD45RA CD4 lymphocyte act	18.7	Coronary artery SMC rest	9.9
CD45RO CD4 lymphocyte act	0.6	Coronary artery SMC TNFalpha + IL-1beta	3.5
CD8 lymphocyte act	1.2	Astrocytes rest	100.0
Secondary CD8 lymphocyte rest	0.9	Astrocytes TNFalpha + IL-1beta	65.5
Secondary CD8 lymphocyte act	0.2	KU-812 (Basophil) rest	11.7
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	8.5
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.3	CCD1106 (Keratinocytes) none	2.0
LAK cells rest	4.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	2.0
LAK cells IL-2	1.2	Liver cirrhosis	3.6
LAK cells IL-2+IL-12	0.4	Lupus kidney	13.6
LAK cells IL-2+IFN gamma	2.1	NCI-H292 none	11.0
LAK cells IL-2+ IL-18	1.2	NCI-H292 IL-4	25.0
LAK cells PMA/ionomycin	2.0	NCI-H292 IL-9	15.6
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	12.5
Two Way MLR 3 day	5.2	NCI-H292 IFN gamma	4.6
Two Way MLR 5 day	2.7	HPAEC none	1.5
Two Way MLR 7 day	1.8	HPAEC TNF alpha + IL-1 beta	2.5
PBMC rest	0.2	Lung fibroblast none	80.1
PBMC PWM	1.9	Lung fibroblast TNF alpha + IL-1 beta	22.7
PBMC PHA-L	0.3	Lung fibroblast IL-4	97.3
Ramos (B cell) none	2.1	Lung fibroblast IL-9	17.6
B lymphocytes PWM	0.7	Lung fibroblast IFN gamma	50.7

B lymphocytes CD40L and IL-4	0.6	Dermal fibroblast CCD1070 rest	94.6
EOL-1 dbcAMP	4.9	Dermal fibroblast CCD1070 TNF alpha	43.2
EOL-1 dbcAMP PMA/ionomycin	1.2	Dermal fibroblast CCD1070 IL-1 beta	31.2
Dendritic cells none	12.8	Dermal fibroblast IFN gamma	14.2
Dendritic cells LPS	1.3	Dermal fibroblast IL-4	95.9
Dendritic cells anti-CD40	11.4	IBD Colitis 2	1.2
Monocytes rest	0.5	IBD Crohn's	9.1
Monocytes LPS	1.3	Colon	60.7
Macrophages rest	13.6	Lung	8.0
Macrophages LPS	2.8	Thymus	39.2
HUVEC none	1.0	Kidney	10.4
HUVEC starved	1.6		

CNS_neurodegeneration_v1.0 Summary: Ag3337 - This panel confirms the expression of this gene at low to moderate levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders

General_screening_panel_v1.4 Summary: Ag3337 - This gene is expressed in almost all samples on this panel. This gene is expressed at moderate levels in the CNS. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

In addition, this gene is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

Panel 4D Summary: Ag3337 This gene is most highly expressed in resting astrocytes

expression or function of this gene may be effective in the treatment of pathological and inflammatory lung and skin diseases, such as psoriasis, asthma, emphysema, and allergies.

Z. CG57551-01: NAC-1 Like Gene

Expression of gene CG57551-01 was assessed using the primer-probe set Ag3282, described in Table ZA. Results of the RTQ-PCR runs are shown in Tables ZB, ZC and ZD.

Table ZA. Probe Name Ag3282

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -cagatcctcagcttctgctaca-3'	22	269	469
Probe	TET-5' -accagttcctgctcatgtacacggct-3' - TAMRA	26	318	470
Reverse	5' -atctcctggatctgcaggaa-3'	20	347	471

Table ZB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3282, Run 210060482	Tissue Name	Rel. Exp.(%) Ag3282, Run 210060482
AD 1 Hippo	22.8	Control (Path) 3 Temporal Ctx	9.7
AD 2 Hippo	49.0	Control (Path) 4 Temporal Ctx	24.3
AD 3 Hippo	11.5	AD 1 Occipital Ctx	16.5
AD 4 Hippo	12.3	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	66.9	AD 3 Occipital Ctx	10.2
AD 6 Hippo	59.9	AD 4 Occipital Ctx	18.2
Control 2 Hippo	49.3	AD 5 Occipital Ctx	9.5
Control 4 Hippo	18.7	AD 6 Occipital Ctx	41.5
Control (Path) 3 Hippo	6.3	Control 1 Occipital Ctx	6.8
AD 1 Temporal Ctx	19.2	Control 2 Occipital Ctx	91.4
AD 2 Temporal Ctx	40.3	Control 3 Occipital Ctx	16.3
AD 3 Temporal Ctx	14.3	Control 4 Occipital Ctx	12.2
AD 5 Int Temporal Ctx	66.0	Control (Path) 2 Occipital Ctx	9.2

AD 5 SupTemporal Ctx	37.4	Control (Path) 3 Occipital Ctx	5.3
AD 6 Inf Temporal Ctx	36.1	Control (Path) 4 Occipital Ctx	15.8
AD 6 Sup Temporal Ctx	34.4	Control 1 Parietal Ctx	11.7
Control 1 Temporal Ctx	10.0	Control 2 Parietal Ctx	34.2
Control 2 Temporal Ctx	74.7	Control 3 Parietal Ctx	23.3
Control 3 Temporal Ctx	15.0	Control (Path) 1 Parietal Ctx	72.7
Control 4 Temporal Ctx	15.5	Control (Path) 2 Parietal Ctx	21.6
Control (Path) 1 Temporal Ctx	74.2	Control (Path) 3 Parietal Ctx	5.5
Control (Path) 2 Temporal Ctx	31.2	Control (Path) 4 Parietal Ctx	35.8

Table ZC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3282, Run 216512995	Tissue Name	Rel. Exp.(%) Ag3282, Run 216512995
Adipose	1.8	Renal ca. TK-10	22.7
Melanoma* Hs688(A).T	16.3	Bladder	6.3
Melanoma* Hs688(B).T	25.0	Gastric ca. (liver met.) NCI-N87	47.0
Melanoma* M14	25.3	Gastric ca. KATO III	45.7
Melanoma* LOXIMVI	21.6	Colon ca. SW-948	19.3
Melanoma* SK-MEL-5	17.0	Colon ca. SW480	50.3
Squamous cell carcinoma SCC-4	24.7	Colon ca.* (SW480 met) SW620	25.9
Testis Pool	6.1	Colon ca. HT29	17.7
Prostate ca.* (bone met) PC-3	67.8	Colon ca. HCT-116	100.0
Prostate Pool	3.5	Colon ca. CaCo-2	29.1
Placenta	9.6	Colon cancer tissue	14.0
		Colon ca. SW1116	12.7
		Colon ca. SW1116	12.7
		Colon ca. SW-48	5.8
Ovarian ca. SK-OV-3	65.5		

Ovarian ca. OVCAR-4	35.8	Colon Pool	4.9
Ovarian ca. OVCAR-5	37.6	Small Intestine Pool	2.4
Ovarian ca. IGROV-1	28.9	Stomach Pool	3.3
Ovarian ca. OVCAR-8	14.2	Bone Marrow Pool	1.5
Ovary	3.9	Fetal Heart	3.0
Breast ca. MCF-7	42.3	Heart Pool	2.2
Breast ca. MDA-MB-231	69.7	Lymph Node Pool	5.6
Breast ca. BT 549	51.4	Fetal Skeletal Muscle	1.5
Breast ca. T47D	86.5	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	26.4	Spleen Pool	2.8
Breast Pool	4.6	Thymus Pool	3.8
Trachea	8.7	CNS cancer (glio/astro) U87-MG	60.3
Lung	0.2	CNS cancer (glio/astro) U-118-MG	100.0
Fetal Lung	6.3	CNS cancer (neuro;met) SK-N-AS	47.3
Lung ca. NCI-N417	8.4	CNS cancer (astro) SF-539	22.8
Lung ca. LX-1	17.3	CNS cancer (astro) SNB-75	47.3
Lung ca. NCI-H146	15.3	CNS cancer (glio) SNB-19	29.3
Lung ca. SHP-77	16.5	CNS cancer (glio) SF-295	49.3
Lung ca. A549	27.2	Brain (Amygdala) Pool	6.9
Lung ca. NCI-H526	6.1	Brain (cerebellum)	15.1
Lung ca. NCI-H23	25.9	Brain (fetal)	9.2
Lung ca. NCI-H460	8.0	Brain (Hippocampus) Pool	8.9
Lung ca. HOP-62	11.9	Cerebral Cortex Pool	13.4
Lung ca. NCI-H522	21.9	Brain (Substantia nigra) Pool	15.3
Liver	1.7	Brain (Thalamus) Pool	11.5
Fetal Liver	9.8	Brain (whole)	12.6
Fetal Kidney	.	Pituitary gland Pool	.
Renal ca. 786-0	42.0	Salivary Gland	4.0

Renal ca. A498	16.7	Thyroid (female)	3.6
Renal ca. ACHN	13.9	Pancreatic ca. CAPAN2	15.5
Renal ca. UO-31	17.4	Pancreas Pool	6.6

Table ZD, Panel 4D

Tissue Name	Rel. Exp.(%) Ag3282, Run 164634321	Tissue Name	Rel. Exp.(%) Ag3282, Run 164634321
Secondary Th1 act	52.9	HUVEC IL-1beta	13.6
Secondary Th2 act	67.8	HUVEC IFN gamma	42.9
Secondary Tr1 act	75.3	HUVEC TNF alpha + IFN gamma	37.1
Secondary Th1 rest	8.4	HUVEC TNF alpha + IL4	42.6
Secondary Th2 rest	11.4	HUVEC IL-11	25.9
Secondary Tr1 rest	12.2	Lung Microvascular EC none	41.2
Primary Th1 act	53.6	Lung Microvascular EC TNFalpha + IL-1beta	36.3
Primary Th2 act	44.4	Microvascular Dermal EC none	50.3
Primary Tr1 act	60.7	Microvascular Dermal EC TNFalpha + IL-1beta	33.0
Primary Th1 rest	37.6	Bronchial epithelium TNFalpha + IL1beta	51.4
Primary Th2 rest	15.8	Small airway epithelium none	23.3
Primary Tr1 rest	18.3	Small airway epithelium TNFalpha + IL-1beta	71.7
CD45RA CD4 lymphocyte act	33.0	Coronary artery SMC rest	43.5
CD45RO CD4 lymphocyte act	54.7	Coronary artery SMC TNFalpha + IL-1beta	31.0
CD8 lymphocyte act	42.9	Astrocytes rest	38.4
Secondary CD8 lymphocyte rest	50.3	Astrocytes TNFalpha + IL-1beta	37.1
Secondary CD8 lymphocyte act	32.5	KU-812 (Basophil) rest	36.1
CD4 lymphocyte none	2.4	KU-812 (Basophil) PMA/ionomycin	90.8
Primary Th1 Th2 Tr1 rest		CD110C (Koripia)	
Primary Th1 Th2 Tr1 act		TNFalpha + IL-1beta	
LAK cells IL-2	41.2	Liver cirrhosis	2.9

LAK cells IL-2+IL-12	29.5	Lupus kidney	2.2
LAK cells IL-2+IFN gamma	36.3	NCI-H292 none	38.4
LAK cells IL-2+ IL-18	34.2	NCI-H292 IL-4	66.9
LAK cells PMA/ionomycin	11.8	NCI-H292 IL-9	62.4
NK Cells IL-2 rest	29.3	NCI-H292 IL-13	65.1
Two Way MLR 3 day	21.9	NCI-H292 IFN gamma	48.3
Two Way MLR 5 day	27.7	HPAEC none	31.2
Two Way MLR 7 day	27.0	HPAEC TNF alpha + IL-1 beta	37.6
PBMC rest	6.5	Lung fibroblast none	35.6
PBMC PWM	89.5	Lung fibroblast TNF alpha + IL-1 beta	20.7
PBMC PHA-L	53.6	Lung fibroblast IL-4	63.3
Ramos (B cell) none	40.6	Lung fibroblast IL-9	55.5
Ramos (B cell) ionomycin	56.3	Lung fibroblast IL-13	44.8
B lymphocytes PWM	100.0	Lung fibroblast IFN gamma	71.2
B lymphocytes CD40L and IL-4	41.2	Dermal fibroblast CCD1070 rest	78.5
EOL-1 dbcAMP	50.0	Dermal fibroblast CCD1070 TNF alpha	88.9
EOL-1 dbcAMP PMA/ionomycin	46.3	Dermal fibroblast CCD1070 IL-1 beta	49.7
Dendritic cells none	33.2	Dermal fibroblast IFN gamma	21.5
Dendritic cells LPS	26.1	Dermal fibroblast IL-4	43.8
Dendritic cells anti-CD40	29.9	IBD Colitis 2	1.2
Monocytes rest	17.1	IBD Crohn's	1.8
Monocytes LPS	14.0	Colon	15.4
Macrophages rest	59.0	Lung	16.6
Macrophages LPS	29.1	Thymus	15.6
HUVEC none	35.1	Kidney	18.9
HUVEC starved	62.0		

CNS_neurodegeneration_v1.0 Summary: Ag3282 - This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no

trans and those of non-demented controls in this experiment. Please see Panel 1 for a

discussion of the potential utility of this gene in treatment of central nervous system disorders

General_screening_panel_v1.4 Summary: Ag3282 Highest expression of this gene is seen in a brain cancer cell line (CT=24.3). This gene appears to be expressed more highly in the cancer cell lines than in the normal tissue samples on this panel and may be involved in cellular growth and proliferation. Based on this expression profile, this gene may be involved in gastric, pancreatic, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene is also expressed at high levels in all regions of the CNS examined. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

In addition, this gene product is expressed in adipose, pancreas, adrenal, thyroid, pituitary, fetal skeletal muscle, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

Furthermore, this gene is more highly expressed in fetal skeletal muscle (CT=30.4) and liver (CT=27) when compared to expression in the adult skeletal muscle (CT>35) and liver (CT=30) may be useful for the differentiation of the fetal and adult sources of this tissue.

Panel 4D Summary: Ag3282 This gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease. Highest expression is seen in pokeweed mitogen stimulated B lymphocytes (CT=25.7). In addition, expression is seen in members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in Panel 1.4 and also suggests a role for the gene product in cell

improvement of the symptoms of patients suffering from autoimmune and inflammatory

diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

AA. CG57411-01: KELCH-LIKE PROTEIN KLHL3C

Expression of gene CG57411-01 was assessed using the primer-probe set Ag3229, described in Table AAA. Results of the RTQ-PCR runs are shown in Tables AAB, AAC, AAD and AAE.

Table AAA. Probe Name Ag3229

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gcagcgagctctaccacat-3'	19	287	472
Probe	TET-5'-aaggccttcgcgctgcagatcct-3'- TAMRA	23	310	473
Reverse	5'-aagtcgtccttggagatgct-3'	20	364	474

Table AAB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3229, Run 209862301	Tissue Name	Rel. Exp.(%) Ag3229, Run 209862301
AD 1 Hippo	16.3	Control (Path) 3 Temporal Ctx	8.0
AD 2 Hippo	34.6	Control (Path) 4 Temporal Ctx	35.8
AD 3 Hippo	15.9	AD 1 Occipital Ctx	18.6
AD 4 Hippo	6.9	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	100.0	AD 3 Occipital Ctx	11.7
AD 6 Hippo	35.4	AD 4 Occipital Ctx	17.7
Control 2 Hippo	31.2	AD 5 Occipital Ctx	49.7
Control 4 Hippo	12.1	AD 6 Occipital Ctx	14.2
Control (Path) 3 Hippo	6.2	Control 1 Occipital Ctx	3.3
AD 1 Temporal Ctx	21.6	Control 2 Occipital Ctx	69.3
AD 3 Temporal Ctx	14.1	Control 4 Occipital Ctx	12.5

AD 4 Temporal Ctx	16.8	Control (Path) 1 Occipital Ctx	72.2
AD 5 Inf Temporal Ctx	71.7	Control (Path) 2 Occipital Ctx	13.7
AD 5 Sup Temporal Ctx	32.3	Control (Path) 3 Occipital Ctx	6.3
AD 6 Inf Temporal Ctx	30.6	Control (Path) 4 Occipital Ctx	16.8
AD 6 Sup Temporal Ctx	33.9	Control 1 Parietal Ctx	8.6
Control 1 Temporal Ctx	4.4	Control 2 Parietal Ctx	39.8
Control 2 Temporal Ctx	56.6	Control 3 Parietal Ctx	21.5
Control 3 Temporal Ctx	19.6	Control (Path) 1 Parietal Ctx	66.4
Control 3 Temporal Ctx	14.2	Control (Path) 2 Parietal Ctx	26.8
Control (Path) 1 Temporal Ctx	62.0	Control (Path) 3 Parietal Ctx	5.2
Control (Path) 2 Temporal Ctx	36.1	Control (Path) 4 Parietal Ctx	54.3

Table AAC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3229, Run 214439727	Tissue Name	Rel. Exp.(%) Ag3229, Run 214439727
Adipose	6.0	Renal ca. TK-10	20.4
Melanoma* Hs688(A).T	8.1	Bladder	6.7
Melanoma* Hs688(B).T	13.5	Gastric ca. (liver met.) NCI-N87	11.2
Melanoma* M14	2.1	Gastric ca. KATO III	59.5
Melanoma* LOXIMVI	24.8	Colon ca. SW-948	0.6
Melanoma* SK- MEL-5	20.7	Colon ca. SW480	31.6
Squamous cell carcinoma SCC-4	6.7	Colon ca.* (SW480 met) SW620	4.7
Testis Pool	3.0	Colon ca. HT29	2.7
Prostate ca * (bone			
Placenta	1.4	Colon cancer tissue	1.2
Uterus Pool	5.8	Colon ca. SW1116	3.3

Ovarian ca. OVCAR-3	40.9	Colon ca. Colo-205	5.4
Ovarian ca. SK-OV-3	17.7	Colon ca. SW-48	3.3
Ovarian ca. OVCAR-4	11.9	Colon Pool	25.0
Ovarian ca. OVCAR-5	84.1	Small Intestine Pool	14.9
Ovarian ca. IGROV-1	2.0	Stomach Pool	6.4
Ovarian ca. OVCAR-8	8.1	Bone Marrow Pool	9.7
Ovary	8.7	Fetal Heart	1.7
Breast ca. MCF-7	0.9	Heart Pool	10.7
Breast ca. MDA-MB-231	30.1	Lymph Node Pool	21.8
Breast ca. BT 549	8.1	Fetal Skeletal Muscle	4.2
Breast ca. T47D	100.0	Skeletal Muscle Pool	8.7
Breast ca. MDA-N	0.0	Spleen Pool	10.4
Breast Pool	22.4	Thymus Pool	11.2
Trachea	10.4	CNS cancer (glio/astro) U87-MG	55.5
Lung	1.7	CNS cancer (glio/astro) U-118-MG	44.8
Fetal Lung	6.7	CNS cancer (neuro;met) SK-N-AS	5.8
Lung ca. NCI-N417	11.7	CNS cancer (astro) SF-539	0.4
Lung ca. LX-1	37.1	CNS cancer (astro) SNB-75	5.0
Lung ca. NCI-H146	6.2	CNS cancer (glio) SNB-19	2.9
Lung ca. SHP-77	61.1	CNS cancer (glio) SF-295	39.0
Lung ca. A549	6.3	Brain (Amygdala) Pool	8.4
Lung ca. NCI-H526	8.7	Brain (cerebellum)	22.2
Lung ca. NCI-H23	6.3	Brain (fetal)	48.6
Lung ca. NCI-H460	2.9	Brain (Hippocampus) Pool	8.5
Lung ca. HOP-62	8.1	Cerebral Cortex Pool	20.7
Brain (Cerebellum) Pool			
Brain (Hippocampus) Pool			
Fetal Liver	1.8	Brain (whole)	11.5

Liver ca. HepG2	0.2	Spinal Cord Pool	3.3
Kidney Pool	26.8	Adrenal Gland	29.9
Fetal Kidney	10.2	Pituitary gland Pool	10.7
Renal ca. 786-0	7.5	Salivary Gland	4.1
Renal ca. A498	4.0	Thyroid (female)	1.1
Renal ca. ACHN	11.9	Pancreatic ca. CAPAN2	1.0
Renal ca. UO-31	15.3	Pancreas Pool	28.7

Table AAD. Panel 2.2

Tissue Name	Rel. Exp.(%) Ag3229, Run 174442765	Tissue Name	Rel. Exp.(%) Ag3229, Run 174442765
Normal Colon	15.5	Kidney Margin (OD04348)	100.0
Colon cancer (OD06064)	31.9	Kidney malignant cancer (OD06204B)	10.7
Colon Margin (OD06064)	20.6	Kidney normal adjacent tissue (OD06204E)	11.6
Colon cancer (OD06159)	6.0	Kidney Cancer (OD04450-01)	38.4
Colon Margin (OD06159)	12.7	Kidney Margin (OD04450-03)	17.4
Colon cancer (OD06297-04)	3.7	Kidney Cancer 8120613	0.0
Colon Margin (OD06297-05)	22.4	Kidney Margin 8120614	6.0
CC Gr.2 ascend colon (ODO3921)	6.5	Kidney Cancer 9010320	12.0
CC Margin (ODO3921)	10.5	Kidney Margin 9010321	9.9
Colon cancer metastasis (OD06104)	8.6	Kidney Cancer 8120607	47.3
Lung Margin (OD06104)	6.2	Kidney Margin 8120608	5.6
Colon mets to lung (OD04451-01)	31.0	Normal Uterus	48.3
Lung Margin (OD04451-02)	39.5	Uterine Cancer 064011	14.9
Normal Prostate	41.2	Normal Thyroid	2.6
Prostate Metastasis (OD04410)		Thyroid Cancer A302152	
Normal Ovary	23.2	Thyroid Margin	2.7

		A302153	
Ovarian cancer (OD06283-03)	7.2	Normal Breast	46.0
Ovarian Margin (OD06283-07)	17.8	Breast Cancer (OD04566)	5.9
Ovarian Cancer 064008	22.2	Breast Cancer 1024	27.4
Ovarian cancer (OD06145)	9.0	Breast Cancer (OD04590-01)	19.5
Ovarian Margin (OD06145)	13.4	Breast Cancer Mets (OD04590-03)	13.5
Ovarian cancer (OD06455-03)	6.3	Breast Cancer Metastasis (OD04655-05)	12.2
Ovarian Margin (OD06455-07)	12.9	Breast Cancer 064006	8.1
Normal Lung	14.5	Breast Cancer 9100266	3.0
Invasive poor diff. lung adeno (ODO4945-01)	5.0	Breast Margin 9100265	3.4
Lung Margin (ODO4945-03)	37.4	Breast Cancer A209073	11.2
Lung Malignant Cancer (OD03126)	9.6	Breast Margin A2090734	61.1
Lung Margin (OD03126)	14.2	Breast cancer (OD06083)	4.7
Lung Cancer (OD05014A)	4.9	Breast cancer node metastasis (OD06083)	12.7
Lung Margin (OD05014B)	39.0	Normal Liver	2.8
Lung cancer (OD06081)	17.4	Liver Cancer 1026	13.6
Lung Margin (OD06081)	32.3	Liver Cancer 1025	12.9
Lung Cancer (OD04237-01)	4.2	Liver Cancer 6004-T	13.2
Lung Margin (OD04237-02)	24.7	Liver Tissue 6004-N	1.3
Ocular Melanoma Metastasis	12.9	Liver Cancer 6005-T	43.2
Ocular Melanoma Margin (Liver)	10.7	Liver Tissue 6005-N	4.8
Melanoma Metastasis	52.9	Liver Cancer 064003	39.5
Melanoma Margin			
Kidney Ca. Nuclea. grade 2 (OD04338)	40.3	Bladder Cancer A302173	4.2

Kidney Margin (OD04338)	7.5	Normal Stomach	31.4
Kidney Ca Nuclear grade 1/2 (OD04339)	82.4	Gastric Cancer 9060397	1.2
Kidney Margin (OD04339)	13.2	Stomach Margin 9060396	7.1
Kidney Ca, Clear cell type (OD04340)	8.3	Gastric Cancer 9060395	7.4
Kidney Margin (OD04340)	24.7	Stomach Margin 9060394	10.9
Kidney Ca, Nuclear grade 3 (OD04348)	13.1	Gastric Cancer 064005	10.4

Table AAE. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3229, Run 164389704	Tissue Name	Rel. Exp.(%) Ag3229, Run 164389704
Secondary Th1 act	3.4	HUVEC IL-1beta	20.0
Secondary Th2 act	4.8	HUVEC IFN gamma	32.5
Secondary Tr1 act	2.1	HUVEC TNF alpha + IFN gamma	26.6
Secondary Th1 rest	1.2	HUVEC TNF alpha + IL4	35.1
Secondary Th2 rest	2.0	HUVEC IL-11	17.6
Secondary Tr1 rest	4.5	Lung Microvascular EC none	34.2
Primary Th1 act	17.7	Lung Microvascular EC TNFalpha + IL-1beta	49.0
Primary Th2 act	5.3	Microvascular Dermal EC none	30.6
Primary Tr1 act	25.9	Microvascular Dermal EC TNFalpha + IL-1beta	38.7
Primary Th1 rest	14.0	Bronchial epithelium TNFalpha + IL1beta	46.7
Primary Th2 rest	6.5	Small airway epithelium none	22.1
Primary Tr1 rest	22.1	Small airway epithelium TNFalpha + IL-1beta	97.9
CD45RA CD4 lymphocyte act	12.7	Coronary artery SMC rest	31.2
CD45RO CD4		Coronary artery SMC	
Secondary CD8 lymphocyte rest	4.2	Astrocytes TNFalpha IL-1beta	8.0

Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.8
CD4 lymphocyte none	5.6	KU-812 (Basophil) PMA/ionomycin	2.9
2ry Th1/Th2/Tr1_anti-CD95 CH11	3.7	CCD1106 (Keratinocytes) none	6.2
LAK cells rest	5.9	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	6.0
LAK cells IL-2	3.0	Liver cirrhosis	15.5
LAK cells IL-2+IL-12	6.2	Lupus kidney	12.2
LAK cells IL-2+IFN gamma	10.7	NCI-H292 none	30.8
LAK cells IL-2+ IL-18	5.0	NCI-H292 IL-4	49.7
LAK cells PMA/ionomycin	4.0	NCI-H292 IL-9	43.5
NK Cells IL-2 rest	1.9	NCI-H292 IL-13	31.6
Two Way MLR 3 day	9.0	NCI-H292 IFN gamma	17.7
Two Way MLR 5 day	3.3	HPAEC none	18.0
Two Way MLR 7 day	1.2	HPAEC TNF alpha + IL-1 beta	58.2
PBMC rest	0.8	Lung fibroblast none	40.6
PBMC PWM	10.7	Lung fibroblast TNF alpha + IL-1 beta	11.0
PBMC PHA-L	10.2	Lung fibroblast IL-4	100.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	55.1
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	78.5
B lymphocytes PWM	23.3	Lung fibroblast IFN gamma	82.4
B lymphocytes CD40L and IL-4	18.6	Dermal fibroblast CCD1070 rest	45.4
EOL-1 dbcAMP	1.8	Dermal fibroblast CCD1070 TNF alpha	36.3
EOL-1 dbcAMP PMA/ionomycin	2.0	Dermal fibroblast CCD1070 IL-1 beta	23.8
Dendritic cells none	5.9	Dermal fibroblast IFN gamma	4.6
Dendritic cells LPS	8.0	Dermal fibroblast IL-4	16.6
Dendritic cells anti-CD40	3.3	IBD Colitis 2	6.2
Macrophages rest		Lung	
Macrophages LPS	1.4	Thymus	20.6

HUVEC none	35.1	Kidney	20.9
HUVEC starved	58.2		

CNS_neurodegeneration_v1.0 Summary: Ag3229 - This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3229 - Highest levels of expression of this gene are seen in breast cancer cell line T47D (CT=28.5). Based on expression in this panel, this gene may be involved in gastric, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

This gene product is also expressed in adipose, pancreas, adrenal, thyroid, pituitary, skeletal muscle, and heart. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

In addition, this gene is expressed at low to moderate levels in all regions of the CNS examined. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 2.2 Summary: Ag3229 Highest expression of the CG57411-01 gene is seen in the kidney (CT=32.2). In addition, significant levels of expression are seen in samples derived from normal lung and breast. Expression in these normal tissues is also higher than in the corresponding malignant tissue. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of lung, breast and kidney cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of lung, breast and kidney cancer

FIGURE 2 SUMMARY: Ag3229 Significant levels of expression are seen in activated-NC1 treated lung fibroblasts (CT=31.3)

H292 mucoepidermoid cells as well as untreated NCI-H292 cells. Moderate expression is also detected in IL-9, IL-13 and IFN gamma activated lung fibroblasts, human pulmonary aortic endothelial cells (treated and untreated), small airway epithelium (treated and untreated), treated bronchial epithelium and lung microvascular endothelial cells (treated and untreated). The expression of this gene in cells derived from or within the lung suggests that this gene may be involved in normal conditions as well as pathological and inflammatory lung disorders that include chronic obstructive pulmonary disease, asthma, allergy and emphysema. Moderate/low expression of this gene is also detected in treated and untreated HUVECs (endothelial cells) and coronary artery smooth muscle cells (treated and untreated) and normal tissues that include lung, colon, thymus and kidney. Expression in the various immune cell types and tissue samples suggests that therapeutic modulation of this gene product may ameliorate symptoms associated with infectious conditions as well as inflammatory and autoimmune disorders that include psoriasis, allergy, asthma, inflammatory bowel disease, rheumatoid arthritis and osteoarthritis.

AB. CG57399-01 and CG57399-03: PHOSPHOLIPASE ADRAB-B PRECURSOR

Expression of gene CG57399-01 and variant CG57399-03 was assessed using the primer-probe sets Ag3952 and Ag3226, described in Tables ABA and ABB. Results of the RTQ-PCR runs are shown in Tables ABC and ABD.

Table ABA. Probe Name Ag3952

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctgtgtccctgtgtcctgaa-3'	20	1633	475
Probe	TET-5'-tcaacagaacttgctaccctcatcga-3'-TAMRA	26	1666	476
Reverse	5'-gtgggtcttctcctgaaacttc-3'	22	1701	477

Table ABB. Probe Name Ag3226

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gatgatectcaggtcactgtgt-3'	22	1617	478
Probe	TET-5'-ccctgtgtcctgaagtttgatgataactca-3'-TAMRA	30	1639	479

Table ABC. Amplification sensitivity (primer sets)

Tissue Name	Rel. Exp.(%) Ag3952, Run 213856126	Tissue Name	Rel. Exp.(%) Ag3952, Run 213856126
Adipose	9.0	Renal ca. TK-10	15.0
Melanoma* Hs688(A).T	3.0	Bladder	22.7
Melanoma* Hs688(B).T	3.4	Gastric ca. (liver met.) NCI-N87	13.0
Melanoma* M14	0.9	Gastric ca. KATO III	75.3
Melanoma* LOXIMVI	11.7	Colon ca. SW-948	4.3
Melanoma* SK- MEL-5	1.5	Colon ca. SW480	97.3
Squamous cell carcinoma SCC-4	8.7	Colon ca.* (SW480 met) SW620	4.4
Testis Pool	12.8	Colon ca. HT29	0.4
Prostate ca.* (bone met) PC-3	10.5	Colon ca. HCT-116	1.2
Prostate Pool	12.9	Colon ca. CaCo-2	60.7
Placenta	5.1	Colon cancer tissue	28.7
Uterus Pool	6.5	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	7.3	Colon ca. Colo-205	0.9
Ovarian ca. SK-OV- 3	26.4	Colon ca. SW-48	26.1
Ovarian ca. OVCAR-4	1.9	Colon Pool	18.8
Ovarian ca. OVCAR-5	6.7	Small Intestine Pool	5.3
Ovarian ca. IGROV- 1	9.2	Stomach Pool	7.9
Ovarian ca. OVCAR-8	4.2	Bone Marrow Pool	8.4
Ovary	10.0	Fetal Heart	1.2
Breast ca. MCF-7	0.4	Heart Pool	5.7
Breast ca. MDA- MB-231	92.0	Lymph Node Pool	32.1
Breast ca. BT 549	5.5	Fetal Skeletal Muscle	1.2
Breast ca. T47D	2.5	Skeletal Muscle Pool	4.7
Breast ca. MDA-N	1.6	Spleen Pool	18.2
Breast Pool	19.6	Thymus Pool	19.3

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Fetal Lung	8.3	CNS cancer (neuro;met) SK-N-AS	0.9
Lung ca. NCI-N417	0.9	CNS cancer (astro) SF-539	7.6
Lung ca. LX-1	27.2	CNS cancer (astro) SNB-75	17.1
Lung ca. NCI-H146	10.7	CNS cancer (glio) SNB-19	6.8
Lung ca. SHP-77	47.3	CNS cancer (glio) SF-295	5.7
Lung ca. A549	5.1	Brain (Amygdala) Pool	7.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	3.2
Lung ca. NCI-H23	4.1	Brain (fetal)	19.3
Lung ca. NCI-H460	0.5	Brain (Hippocampus) Pool	13.1
Lung ca. HOP-62	2.7	Cerebral Cortex Pool	14.8
Lung ca. NCI-H522	1.3	Brain (Substantia nigra) Pool	6.3
Liver	0.0	Brain (Thalamus) Pool	15.2
Fetal Liver	1.7	Brain (whole)	10.4
Liver ca. HepG2	0.5	Spinal Cord Pool	5.3
Kidney Pool	21.2	Adrenal Gland	100.0
Fetal Kidney	1.6	Pituitary gland Pool	4.3
Renal ca. 786-0	1.7	Salivary Gland	3.4
Renal ca. A498	1.3	Thyroid (female)	14.5
Renal ca. ACHN	4.3	Pancreatic ca. CAPAN2	1.7
Renal ca. UO-31	17.4	Pancreas Pool	24.5

Table ABD. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3226, Run 167994701	Tissue Name	Rel. Exp.(%) Ag3226, Run 167994701
Liver adenocarcinoma	2.5	Kidney (fetal)	16.3
Pancreas	0.0	Renal ca. 786-0	0.9
Pancreatic ca. CAPAN 2	0.0	Renal ca. A498	1.4
Adrenal gland	19.6	Renal ca. RXF 393	3.4
Thyroid	16.3	Renal ca. ACHN	1.4
Salivary gland	0.0	Renal ca. UO-31	2.8
Pituitary gland	1.9	Renal ca. TK-10	4.4
Brain (amygdala)	6.7	Liver ca (hepatoblast) HepG2	0.0

Brain (cerebellum)	1.6	Lung	8.8
Brain (hippocampus)	22.2	Lung (fetal)	1.7
Brain (substantia nigra)	3.1	Lung ca. (small cell) LX-1	18.6
Brain (thalamus)	3.2	Lung ca. (small cell) NCI-H69	4.2
Cerebral Cortex	26.2	Lung ca. (s.cell var.) SHP-77	100.0
Spinal cord	3.1	Lung ca. (large cell)NCI-H460	0.0
glio/astro U87-MG	7.5	Lung ca. (non-sm. cell) A549	6.7
glio/astro U-118-MG	4.2	Lung ca. (non-s.cell) NCI-H23	5.7
astrocytoma SW1783	1.2	Lung ca. (non-s.cell) HOP-62	0.0
neuro*; met SK-N-AS	0.0	Lung ca. (non-s.cl) NCI-H522	0.0
astrocytoma SF-539	0.0	Lung ca. (squam.) SW 900	0.9
astrocytoma SNB-75	4.3	Lung ca. (squam.) NCI-H596	3.7
glioma SNB-19	6.0	Mammary gland	6.3
glioma U251	14.1	Breast ca.* (pl.ef) MCF-7	0.0
glioma SF-295	0.0	Breast ca.* (pl.ef) MDA-MB-231	45.4
Heart (fetal)	1.4	Breast ca.* (pl.ef) T47D	4.3
Heart	1.0	Breast ca. BT-549	7.1
Skeletal muscle (fetal)	0.7	Breast ca. MDA-N	0.0
Skeletal muscle	3.2	Ovary	10.9
Bone marrow	3.1	Ovarian ca. OVCAR- 3	0.0
Thymus	5.7	Ovarian ca. OVCAR- 4	2.4
Spleen	7.2	Ovarian ca. OVCAR- 5	5.2
Lymph node	0.0	Ovarian ca. OVCAR- 8	0.0
		Ovarian ca. IGROV-	
Small intestine			
	1.5	Uterus	5.8

Colon ca. SW480	33.2	Placenta	0.0
Colon ca.* SW620(SW480 met)	8.8	Prostate	1.6
Colon ca. HT29	0.0	Prostate ca.* (bone met)PC-3	2.6
Colon ca. HCT-116	0.0	Testis	7.4
Colon ca. CaCo-2	35.4	Melanoma Hs688(A).T	0.0
Colon ca. tissue(ODO3866)	24.5	Melanoma* (met) Hs688(B).T	0.0
Colon ca. HCC-2998	15.7	Melanoma UACC-62	0.0
Gastric ca.* (liver met) NCI-N87	6.4	Melanoma M14	0.0
Bladder	14.6	Melanoma LOX IMVI	0.0
Trachea	4.4	Melanoma* (met) SK-MEL-5	0.0
Kidney	2.4	Adipose	17.3

General_screening_panel_v1.4 Summary: Ag3952 Highest expression of this gene is seen in the adrenal gland (CT=29). Thus, this gene product may be a treatment for Addison's disease and other adrenalopathies. This gene also has low levels of expression in adipose, heart, skeletal muscle, pituitary, thyroid, and pancreas. Therapeutic modulation of this gene product may be important for the diagnosis or treatment of endocrine or metabolic disease, including Types 1 and 2 diabetes, obesity and pancreatitis.

Expression of this gene is also seen in sample derived from colon, gastric, lung and breast cancers. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon, gastric, lung and breast cancers.

Low but significant levels of expression are also seen for all regions of the CNS examined. Thus, this gene product may be useful for treatment of CNS disorders such as Alzheimer's disease, Parkinson's disease, stroke, epilepsy, schizophrenia and multiple sclerosis.

from breast and colon cancers. Overall, expression is consistent with expression seen in Panel

1.4. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of these cancers.

Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon, gastric, lung and breast cancers.

Among metabolic tissues, significant levels of expression are seen in adipose and the adrenal gland. Thus, this gene product may be useful for treatment of obesity, Addison's disease and other adrenalopathies.

In addition, this gene is expressed in the hippocampus, and cerebral cortex. Both these regions of the brain undergo degeneration in Alzheimer's disease. Thus, therapeutic modulation of the expression or function of this gene may be effective in the treatment of this disease or any other neurodegenerative disorders.

AC. CG57399-02: PHOSPHOLIPASE ADRAB-B PRECURSOR

Expression of gene CG57399-02 was assessed using the primer-probe set Ag3952, described in Table ACA. Results of the RTQ-PCR runs are shown in Table ACB. Please note that this gene represents a variant of CG57399-01. This sequence however, only corresponds to probe and primer set Ag3952.

Table ACA. Probe Name Ag3952

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctgtgtccctgtgtcctgaa-3'	20	578	481
Probe	TET-5'-tcaacagaacttgctaccctcatcga-3'- TAMRA	26	611	482
Reverse	5'-gtgggtcttctcctgaaacttc-3'	22	646	483

Table ACB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3952, Run 213856126	Tissue Name	Rel. Exp.(%) Ag3952, Run 213856126
Adipose	9.0	Renal ca. TK-10	15.0
Melanoma*	3.0	Bladder	22.7
MS088(B)	0.9	Gastric ca. KATO III	15.3

Melanoma* LOXIMVI	11.7	Colon ca. SW-948	4.3
Melanoma* SK- MEL-5	1.5	Colon ca. SW480	97.3
Squamous cell carcinoma SCC-4	8.7	Colon ca.* (SW480 met) SW620	4.4
Testis Pool	12.8	Colon ca. HT29	0.4
Prostate ca.* (bone met) PC-3	10.5	Colon ca. HCT-116	1.2
Prostate Pool	12.9	Colon ca. CaCo-2	60.7
Placenta	5.1	Colon cancer tissue	28.7
Uterus Pool	6.5	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	7.3	Colon ca. Colo-205	0.9
Ovarian ca. SK-OV- 3	26.4	Colon ca. SW-48	26.1
Ovarian ca. OVCAR-4	1.9	Colon Pool	18.8
Ovarian ca. OVCAR-5	6.7	Small Intestine Pool	5.3
Ovarian ca. IGROV- 1	9.2	Stomach Pool	7.9
Ovarian ca. OVCAR-8	4.2	Bone Marrow Pool	8.4
Ovary	10.0	Fetal Heart	1.2
Breast ca. MCF-7	0.4	Heart Pool	5.7
Breast ca. MDA- MB-231	92.0	Lymph Node Pool	32.1
Breast ca. BT 549	5.5	Fetal Skeletal Muscle	1.2
Breast ca. T47D	2.5	Skeletal Muscle Pool	4.7
Breast ca. MDA-N	1.6	Spleen Pool	18.2
Breast Pool	19.6	Thymus Pool	19.3
Trachea	10.3	CNS cancer (glio/astro) U87-MG	38.2
Lung	1.2	CNS cancer (glio/astro) U-118-MG	12.2
Fetal Lung	8.3	CNS cancer (neuro;met) SK-N-AS	0.9
Lung ca. NCI-N417	0.9	CNS cancer (astro) SF- 539	7.6

Lung ca. NCI-H147		CNS cancer (glio) SNB-19	
Lung ca. SHP-77	47.3	CNS cancer (glio) SF-	5.7

		295	
Lung ca. A549	5.1	Brain (Amygdala) Pool	7.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	3.2
Lung ca. NCI-H23	4.1	Brain (fetal)	19.3
Lung ca. NCI-H460	0.5	Brain (Hippocampus) Pool	13.1
Lung ca. HOP-62	2.7	Cerebral Cortex Pool	14.8
Lung ca. NCI-H522	1.3	Brain (Substantia nigra) Pool	6.3
Liver	0.0	Brain (Thalamus) Pool	15.2
Fetal Liver	1.7	Brain (whole)	10.4
Liver ca. HepG2	0.5	Spinal Cord Pool	5.3
Kidney Pool	21.2	Adrenal Gland	100.0
Fetal Kidney	1.6	Pituitary gland Pool	4.3
Renal ca. 786-0	1.7	Salivary Gland	3.4
Renal ca. A498	1.3	Thyroid (female)	14.5
Renal ca. ACHN	4.3	Pancreatic ca. CAPAN2	1.7
Renal ca. UO-31	17.4	Pancreas Pool	24.5

General_screening_panel_v1.4 Summary: Ag3952 Highest expression of this gene is seen in the adrenal gland (CT=29). Thus, this gene product may be a treatment for Addison's disease and other adrenalopathies. This gene also has low levels of expression in adipose, heart, skeletal muscle, pituitary, thyroid, and pancreas. Therapeutic modulation of this gene product may be important for the diagnosis or treatment of endocrine or metabolic disease, including Types 1 and 2 diabetes, obesity and pancreatitis.

Expression of this gene is also seen in cell line samples derived from colon, gastric, lung and breast cancers. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon, gastric, lung and breast cancers.

Low but significant levels of expression are also seen for all regions of the CNS examined. Thus, this gene product may be useful for treatment of CNS disorders such as Alzheimer's disease, Parkinson's disease, stroke, epilepsy, schizophrenia and multiple

AD:CG59311-01 ACYL-COENZYME A THIOESTER HYDROLASE dp

Expression of gene CG59311-01, splice variant CG59311-02, and full length clone CG59311-03, was assessed using the primer-probe set Ag3541, described in Table ADA. Results of the RTQ-PCR runs are shown in Tables ADB and ADC.

Table ADA. Probe Name Ag3541

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctcactcaaaggcacaggtaga-3'	22	1199	484
Probe	TET-5'-tggcagcaaattcaaactttcttcca-3'- TAMRA	26	1225	485
Reverse	5'-tttgctgtgcttgacagatttt-3'	22	1269	486

Table ADB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3541, Run 217049294	Tissue Name	Rel. Exp.(%) Ag3541, Run 217049294
Adipose	0.0	Renal ca. TK-10	6.0
Melanoma* Hs688(A).T	0.7	Bladder	3.7
Melanoma* Hs688(B).T	1.6	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	2.7
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	5.4
Testis Pool	3.1	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	1.4	Colon ca. HCT-116	0.6
Prostate Pool	2.3	Colon ca. CaCo-2	0.6
Placenta	0.5	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	2.9	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	0.0	Colon ca. SW-48	0.0
Ovarian ca. IGROV-3	0.0	Stomach Pool	3.1

1			
Ovarian ca. OVCAR-8	1.8	Bone Marrow Pool	1.4
Ovary	2.5	Fetal Heart	9.2
Breast ca. MCF-7	2.4	Heart Pool	3.4
Breast ca. MDA-MB-231	8.0	Lymph Node Pool	3.9
Breast ca. BT 549	4.9	Fetal Skeletal Muscle	4.9
Breast ca. T47D	52.9	Skeletal Muscle Pool	13.5
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	6.7	Thymus Pool	4.7
Trachea	0.9	CNS cancer (glio/astro) U87-MG	0.9
Lung	1.7	CNS cancer (glio/astro) U-118-MG	12.1
Fetal Lung	2.2	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	4.2	CNS cancer (astro) SNB-75	5.2
Lung ca. NCI-H146	2.1	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	6.7	CNS cancer (glio) SF-295	0.7
Lung ca. A549	0.0	Brain (Amygdala) Pool	4.2
Lung ca. NCI-H526	0.0	Brain (cerebellum)	100.0
Lung ca. NCI-H23	10.2	Brain (fetal)	14.7
Lung ca. NCI-H460	3.4	Brain (Hippocampus) Pool	9.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	9.7
Lung ca. NCI-H522	8.5	Brain (Substantia nigra) Pool	3.5
Liver	0.5	Brain (Thalamus) Pool	10.5
Fetal Liver	1.5	Brain (whole)	12.9
Liver ca. HepG2	0.5	Spinal Cord Pool	7.6
Kidney Pool	9.8	Adrenal Gland	10.2
Fetal Kidney	7.9	Pituitary gland Pool	3.1
Renal ca. 786-0	0.0	Salivary Gland	1.7
Renal ca. A498	0.0	Thyroid (female)	0.0

NCI/NIH/DOH
 10/1/00

NCI/NIH/DOH
 10/1/00

Table ADC, Panel 4D

Tissue Name	Rel. Exp.(%) Ag3541, Run 166447041	Tissue Name	Rel. Exp.(%) Ag3541, Run 166447041
Secondary Th1 act	2.7	HUVEC IL-1beta	0.0
Secondary Th2 act	4.1	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	2.1
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	2.7	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	2.3
CD45RO CD4 lymphocyte act	1.7	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	1.8
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	4.2
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	1.4
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	2.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	9.8
LAK cells IL-2	0.0	Liver cirrhosis	22.2
LAK cells IL-2+IL-12	0.0	Lupus kidney	18.4
LAK cells IL-2+IFN			
LAK cells PMA ionomycin	0.0	NCI-H292 IL-9	15.2

NK Cells IL-2 rest	1.7	NCI-H292 IL-13	3.1
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	7.3
Two Way MLR 5 day	5.3	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	1.7
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	5.7
PBMC PHA-L	2.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	2.2	Lung fibroblast IL-13	3.2
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	2.9
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	2.9
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	3.5	Dermal fibroblast IL-4	1.5
Dendritic cells anti-CD40	0.0	IBD Colitis 2	5.4
Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	0.0	Colon	14.1
Macrophages rest	4.5	Lung	0.0
Macrophages LPS	2.1	Thymus	100.0
HUVEC none	0.0	Kidney	2.3
HUVEC starved	2.5		

CNS_neurodegeneration_v1.0 Summary: Ag3541 - Expression of this gene is low/undetectable (CTs > 34.5) across all of the samples on this panel (data not shown).

General_screening_panel_v1.4 Summary: Ag3541 Significant expression of this gene is seen only in cerebellum, fetal brain, the breast cancer cell line T47D, and ovarian cancer cell line OVCAR-5 (CTs=32-35). Therefore, expression of this gene can be used to differentiate

Panel 4D Summary: Ag3541 Significant expression of this gene is seen only in thymus (CT=33.8). Therefore, expression of this gene may be used to identify thymic tissue.

Furthermore, drugs that inhibit the function of this protein may regulate T cell development in the thymus and reduce or eliminate the symptoms of T cell mediated autoimmune or inflammatory diseases, including asthma, allergies, inflammatory bowel disease, lupus erythematosus, or rheumatoid arthritis. Additionally, therapeutics designed against this putative protein may disrupt T cell development in the thymus and function as an immunosuppressant for tissue transplant.

AE. CG59309-01: ACYL-COENZYME A THIOESTER HYDROLASE

Expression of gene CG59309-01 was assessed using the primer-probe set Ag3540, described in Table AEA. Results of the RTQ-PCR runs are shown in Tables AEB, AEC, AED and AEE.

Table AEA. Probe Name Ag3540

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ccacgttggtcttagcttatta-3'	22	649	487
Probe	TET-5'-tgaagatctccccaataacatggaca-3'- TAMRA	26	677	488
Reverse	5'-ttcgaagtactccagggatatg-3'	22	704	489

Table AEB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3540, Run 210638385	Tissue Name	Rel. Exp.(%) Ag3540, Run 210638385
AD 1 Hippo	13.7	Control (Path) 3 Temporal Ctx	8.2
AD 2 Hippo	26.2	Control (Path) 4 Temporal Ctx	34.2
AD 3 Hippo	13.1	AD 1 Occipital Ctx	23.2
AD 4 Hippo	3.4	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	30.4	AD 3 Occipital Ctx	7.8
AD 6 Hippo	55.9	AD 4 Occipital Ctx	15.0
Control 2 Hippo	24.0	AD 5 Occipital Ctx	8.1
Control 4 Hippo	4.5	AD 6 Occipital Ctx	76.3
Control (Path) 3		Control 1 Occipital	
AD 2 Temporal Ctx	19.5	Control 3 Occipital	36.3

		Ctx	
AD 3 Temporal Ctx	4.8	Control 4 Occipital Ctx	3.9
AD 4 Temporal Ctx	15.6	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	36.9	Control (Path) 2 Occipital Ctx	7.6
AD 5 Sup Temporal Ctx	27.4	Control (Path) 3 Occipital Ctx	1.6
AD 6 Inf Temporal Ctx	47.3	Control (Path) 4 Occipital Ctx	16.6
AD 6 Sup Temporal Ctx	64.2	Control 1 Parietal Ctx	8.7
Control 1 Temporal Ctx	7.0	Control 2 Parietal Ctx	20.7
Control 2 Temporal Ctx	53.2	Control 3 Parietal Ctx	27.2
Control 3 Temporal Ctx	19.9	Control (Path) 1 Parietal Ctx	88.9
Control 4 Temporal Ctx	10.5	Control (Path) 2 Parietal Ctx	10.8
Control (Path) 1 Temporal Ctx	68.3	Control (Path) 3 Parietal Ctx	10.1
Control (Path) 2 Temporal Ctx	25.3	Control (Path) 4 Parietal Ctx	47.6

Table AEC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3540, Run 217049291	Tissue Name	Rel. Exp.(%) Ag3540, Run 217049291
Adipose	1.3	Renal ca. TK-10	0.1
Melanoma* Hs688(A).T	0.7	Bladder	1.1
Melanoma* Hs688(B).T	0.5	Gastric ca. (liver met.) NCI-N87	5.6
Melanoma* M14	0.2	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	10.3
Squamous cell		Colon ca * (SW480	
Prostate ca * (Duke met) PC-3	0.8	Colon ca. HCT-116	0.0

Prostate Pool	0.3	Colon ca. CaCo-2	3.5
Placenta	1.4	Colon cancer tissue	1.4
Uterus Pool	0.1	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	1.6	Colon ca. Colo-205	3.3
Ovarian ca. SK-OV-3	3.6	Colon ca. SW-48	1.7
Ovarian ca. OVCAR-4	0.4	Colon Pool	0.2
Ovarian ca. OVCAR-5	23.7	Small Intestine Pool	0.3
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.1
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.2
Ovary	0.1	Fetal Heart	0.4
Breast ca. MCF-7	0.0	Heart Pool	0.2
Breast ca. MDA-MB-231	2.5	Lymph Node Pool	0.3
Breast ca. BT 549	3.0	Fetal Skeletal Muscle	0.1
Breast ca. T47D	100.0	Skeletal Muscle Pool	0.4
Breast ca. MDA-N	0.0	Spleen Pool	0.2
Breast Pool	0.3	Thymus Pool	0.3
Trachea	0.4	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.3
Fetal Lung	0.2	CNS cancer (neuro;met) SK-N-AS	1.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.6
Lung ca. LX-1	3.5	CNS cancer (astro) SNB-75	3.1
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.1	CNS cancer (glio) SF-295	0.2
Lung ca. A549	1.4	Brain (Amygdala) Pool	0.7
Lung ca. NCI-H526	0.7	Brain (cerebellum)	2.1
Lung ca. NCI-H23	1.3	Brain (fetal)	0.5
		Brain (Hippocampus)	0.5
		Cerebral Cortex (fetal)	0.5
Lung ca. NCI-H522	0.0	Brain (Substantia nigra)	1.3

		Pool	
Liver	2.6	Brain (Thalamus) Pool	1.1
Fetal Liver	0.8	Brain (whole)	1.4
Liver ca. HepG2	0.1	Spinal Cord Pool	0.5
Kidney Pool	0.7	Adrenal Gland	0.8
Fetal Kidney	0.6	Pituitary gland Pool	0.1
Renal ca. 786-0	0.0	Salivary Gland	0.2
Renal ca. A498	0.0	Thyroid (female)	0.7
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	9.4
Renal ca. UO-31	1.1	Pancreas Pool	0.9

Table AED. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3540, Run 166447040	Tissue Name	Rel. Exp.(%) Ag3540, Run 166447040
Secondary Th1 act	4.8	HUVEC IL-1beta	1.7
Secondary Th2 act	10.2	HUVEC IFN gamma	0.9
Secondary Tr1 act	12.9	HUVEC TNF alpha + IFN gamma	1.5
Secondary Th1 rest	2.1	HUVEC TNF alpha + IL4	0.8
Secondary Th2 rest	1.4	HUVEC IL-11	1.5
Secondary Tr1 rest	1.6	Lung Microvascular EC none	0.6
Primary Th1 act	4.7	Lung Microvascular EC TNFalpha + IL-1beta	0.8
Primary Th2 act	6.8	Microvascular Dermal EC none	1.5
Primary Tr1 act	7.3	Microvascular Dermal EC TNFalpha + IL-1beta	0.8
Primary Th1 rest	6.6	Bronchial epithelium TNFalpha + IL1beta	1.3
Primary Th2 rest	2.6	Small airway epithelium none	0.6
Primary Tr1 rest	4.2	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	4.1	Coronary artery SMC rest	0.9
CD45RO CD4 lymphocyte act	10.9	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD45RO CD4 lymphocyte rest		IL-1beta	
Secondary CD8	6.0	KU-812 (Basophil) rest	2.2

lymphocyte act			
CD4 lymphocyte none	2.0	KU-812 (Basophil) PMA/ionomycin	10.2
2ry Th1/Th2/Tr1_anti- CD95 CH11	2.4	CCD1106 (Keratinocytes) none	6.8
LAK cells rest	2.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	25.7
LAK cells IL-2	16.2	Liver cirrhosis	12.0
LAK cells IL-2+IL-12	12.8	Lupus kidney	5.1
LAK cells IL-2+IFN gamma	15.6	NCI-H292 none	44.8
LAK cells IL-2+ IL-18	7.4	NCI-H292 IL-4	37.6
LAK cells PMA/ionomycin	3.4	NCI-H292 IL-9	41.2
NK Cells IL-2 rest	9.0	NCI-H292 IL-13	19.8
Two Way MLR 3 day	10.5	NCI-H292 IFN gamma	30.1
Two Way MLR 5 day	7.2	HPAEC none	1.2
Two Way MLR 7 day	8.9	HPAEC TNF alpha + IL-1 beta	3.3
PBMC rest	0.5	Lung fibroblast none	0.9
PBMC PWM	3.8	Lung fibroblast TNF alpha + IL-1 beta	0.7
PBMC PHA-L	1.0	Lung fibroblast IL-4	0.5
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.9
B lymphocytes PWM	10.3	Lung fibroblast IFN gamma	1.2
B lymphocytes CD40L and IL-4	3.8	Dermal fibroblast CCD1070 rest	1.1
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	18.9
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	1.9
Dendritic cells none	14.9	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	8.9	Dermal fibroblast IL-4	1.5
Dendritic cells anti- CD40	7.9	IBD Colitis 2	2.9
Monocytes rest	0.0	IBD Crohn's	1.9
Macrophages LPS		Enthus	100.0
HUVEC none	1.1	Kidney	1.8

HUVEC starved	1.4		
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Table AEE. Panel 5 Islet

Tissue Name	Rel. Exp.(%) Ag3540, Run 242386396	Tissue Name	Rel. Exp.(%) Ag3540, Run 242386396
97457_Patient-02go_adipose	3.3	94709_Donor 2 AM - A_adipose	9.1
97476_Patient-07sk_skeletal muscle	0.8	94710_Donor 2 AM - B_adipose	1.6
97477_Patient-07ut_uterus	0.0	94711_Donor 2 AM - C_adipose	1.4
97478_Patient-07pl_placenta	12.9	94712_Donor 2 AD - A_adipose	2.8
99167_Bayer Patient 1	15.5	94713_Donor 2 AD - B_adipose	5.8
97482_Patient-08ut_uterus	3.4	94714_Donor 2 AD - C_adipose	4.2
97483_Patient-08pl_placenta	3.4	94742_Donor 3 U - A_Mesenchymal Stem Cells	3.0
97486_Patient-09sk_skeletal muscle	100.0	94743_Donor 3 U - B_Mesenchymal Stem Cells	1.1
97487_Patient-09ut_uterus	1.6	94730_Donor 3 AM - A_adipose	4.3
97488_Patient-09pl_placenta	2.6	94731_Donor 3 AM - B_adipose	2.0
97492_Patient-10ut_uterus	3.1	94732_Donor 3 AM - C_adipose	2.0
97493_Patient-10pl_placenta	23.2	94733_Donor 3 AD - A_adipose	10.7
97495_Patient-11go_adipose	0.8	94734_Donor 3 AD - B_adipose	3.0
97496_Patient-11sk_skeletal muscle	0.0	94735_Donor 3 AD - C_adipose	4.0
97497_Patient-11ut_uterus	2.5	77138_Liver_HepG2untreated	0.7
97498_Patient-11pl_placenta	6.7	73556_Heart_Cardiac stromal cells (primary)	0.0
97500_Patient-12go_adipose	6.5	81735_Small Intestine	4.8
97501 Patient-	.	72409 Kidney Proximal	-
Pat. uterus			
97503_Patient-	2.4	90650 Adrenal Adrenocortical	0.6

l2pl_placenta		adenoma	
94721_Donor 2 U - A_Mesenchymal Stem Cells	2.2	72410_Kidney_HRCE	8.0
94722_Donor 2 U - B_Mesenchymal Stem Cells	0.6	72411_Kidney_HRE	8.5
94723_Donor 2 U - C_Mesenchymal Stem Cells	3.1	73139_Uterus_Uterine smooth muscle cells	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3540 - This panel confirms the expression of this gene at low levels in the brain in an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment.

General_screening_panel_v1.4 Summary: Ag3540 This gene is most highly expressed in a breast cancer cell line (CT=27.1). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker to detect the presence of breast cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of breast cancer.

Among metabolic tissues, this gene, an acyl coA thioesterase homolog, has a low level of expression in adipose, adult and fetal liver, adrenal, thyroid and pancreas. Acyl CoA thioesterases have multiple roles in lipid homeostasis. Therefore, therapeutic modulation of this gene product may be a treatment for endocrine and metabolic disease, including Types 1 and 2 diabetes and obesity.

In addition, this gene is expressed in all CNS regions examined. Thus, therapeutic modulation of the expression or function of this gene may be effective in the treatment of neurologic disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, stroke, schizophrenia and multiple sclerosis.

References:

1.

2. Hunt MC, Nousiainen SE, Huttunen MK, Orit KE, Svensson LT, Alexson SE.

Peroxisome proliferator-induced long chain acyl-CoA thioesterases comprise a highly conserved novel multi-gene family involved in lipid metabolism. J Biol Chem. 1999 Nov 26;274(48):34317-26.

Panel 4D Summary: Ag3540 Highest expression of the CG59309-01 gene is seen in the thymus and colon (CTs=31.5). Significant levels of expression are also seen in a cluster of treated and untreated samples derived from the NCI-H292 mucoepidermoid cell line. Thus, expression of this gene could be used as a marker for thymus and colon. Furthermore, therapeutic modulation of the expression or function of this gene may regulate T cell development in the thymus and reduce or eliminate the symptoms of T cell mediated autoimmune or inflammatory diseases, including asthma, allergies, inflammatory bowel disease, lupus erythematosus, or rheumatoid arthritis. Additionally, small molecule or antibody therapeutics designed against this putative protein may disrupt T cell development in the thymus and function as an immunosuppressant for tissue transplant.

Panel 5 Islet Summary: Ag3540 This gene has moderate expression in skeletal muscle, (highest expression CT=30.5). Acyl CoA thioesterases function in peroxisomal fatty acid oxidation. Therefore, therapeutic modulation of this homolog may increase fatty acid oxidation in muscle and be a treatment for Type 2 diabetes and obesity.

References:

1. Hunt MC, Solaas K, Kase BF, Alexson SE. Characterization of an acyl-coA thioesterase that functions as a major regulator of peroxisomal lipid metabolism. J Biol Chem. 2002 Jan 11;277(2):1128-38.

AF. CG57364-01: CG6896

Expression of gene CG57364-01 was assessed using the primer-probe sets Ag3218 and Ag3378, described in Tables AFA and AFB. Results of the RTQ-PCR runs are shown in Tables AFC, AFD, AFE and AFF.

Primers	Sequences	Length	Start Position	SEQ ID NO:
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Forward	5'-ctcctgaagcagggtcctctt-3'	20	249	490
Probe	TET-5'-cctcccagtggtgtccttctggagg-3'- TAMRA	25	270	491
Reverse	5'-gacttcttccagggtcatttcg-3'	21	303	492

Table AFB. Probe Name Ag3378

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ctcctgaagcagggtcctctt-3'	20	249	493
Probe	TET-5'-cctcccagtggtgtccttctggagg-3'- TAMRA	25	270	494
Reverse	5'-gacttcttccagggtcatttcg-3'	21	303	495

Table AFC. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3218, Run 209861784	Rel. Exp.(%) Ag3378, Run 210154573	Tissue Name	Rel. Exp.(%) Ag3218, Run 209861784	Rel. Exp.(%) Ag3378, Run 210154573
AD 1 Hippo	37.6	30.4	Control (Path) 3 Temporal Ctx	17.6	16.7
AD 2 Hippo	31.0	37.6	Control (Path) 4 Temporal Ctx	37.6	31.2
AD 3 Hippo	34.2	21.5	AD 1 Occipital Ctx	56.3	40.3
AD 4 Hippo	40.6	25.3	AD 2 Occipital Ctx (Missing)	0.0	0.0
AD 5 hippo	100.0	69.3	AD 3 Occipital Ctx	43.2	24.1
AD 6 Hippo	62.9	55.9	AD 4 Occipital Ctx	80.1	24.3
Control 2 Hippo	55.1	52.9	AD 5 Occipital	17.9	25.2
Hippo			Occipital Ctx		

Control (Path) 3 Hippo	22.8	26.8	Control 1 Occipital Ctx	27.9	17.4
AD 1 Temporal Ctx	40.3	28.3	Control 2 Occipital Ctx	94.0	64.6
AD 2 Temporal Ctx	83.5	94.6	Control 3 Occipital Ctx	43.5	40.6
AD 3 Temporal Ctx	30.8	24.5	Control 4 Occipital Ctx	20.3	22.5
AD 4 Temporal Ctx	61.1	26.8	Control (Path) 1 Occipital Ctx	79.6	51.4
AD 5 Inf Temporal Ctx	84.7	100.0	Control (Path) 2 Occipital Ctx	34.4	24.7
AD 5 SupTemporal Ctx	55.9	39.8	Control (Path) 3 Occipital Ctx	25.2	16.2
AD 6 Inf Temporal Ctx	47.0	46.0	Control (Path) 4 Occipital Ctx	76.3	45.1
AD 6 Sup Temporal Ctx	63.7	41.2	Control 1 Parietal Ctx	31.0	21.9
Control 1 Temporal Ctx	32.8	18.0	Control 2 Parietal Ctx	67.4	45.1
Control 2 Temporal Ctx	52.1	39.2	Control 3 Parietal Ctx	31.4	29.3
Control 3 Temporal Ctx	34.9	28.1	Control (Path) 1 Parietal Ctx	48.6	58.6
Control 4 Temporal Ctx	62.9	36.3	Control (Path) 2 Parietal Ctx	46.3	27.0
Control (Path) 1 Temporal Ctx	75.8	50.0	Control (Path) 3 Parietal Ctx	26.1	23.8

Control (Path) 1

Parietal Ctx

Table AFD. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3218, Run 168013878	Rel. Exp.(%) Ag3378, Run 165674263	Tissue Name	Rel. Exp.(%) Ag3218, Run 168013878	Rel. Exp.(%) Ag3378, Run 165674263
Liver adenocarcinoma	10.7	20.2	Kidney (fetal)	48.3	13.9
Pancreas	10.8	13.1	Renal ca. 786- 0	15.6	10.4
Pancreatic ca. CAPAN 2	9.6	5.4	Renal ca. A498	19.2	14.9
Adrenal gland	5.1	18.4	Renal ca. RXF 393	39.0	33.2
Thyroid	12.3	33.2	Renal ca. ACHN	12.1	11.3
Salivary gland	5.1	5.5	Renal ca. UO- 31	18.9	17.8
Pituitary gland	21.5	74.7	Renal ca. TK- 10	20.0	10.1
Brain (fetal)	19.5	36.1	Liver	18.0	8.7
Brain (whole)	22.1	29.9	Liver (fetal)	5.5	25.3
Brain (amygdala)	57.4	46.7	Liver ca. (hepatoblast) HepG2	14.2	14.1
Brain (cerebellum)	25.2	23.5	Lung	14.1	18.7
Brain (hippocampus)	28.1	85.9	Lung (fetal)	17.2	4.0
Brain (substantia nigra)	11.5	16.7	Lung ca. (small cell) LX-1	6.5	14.8
Brain (thalamus)	57.0	67.4	Lung ca. (small cell) NCI-H69	20.6	4.8
Cerebral Cortex	75.8	36.9	Lung ca. (s.cell var.) SHP-77	100.0	39.8
Spinal cord	9.7	13.2	Lung ca. (large cell) NCI-H460	5.0	37.1
glioblasto U87-MG	22.8	13.6	Lung ca. (non- sm. cell) A549	27.7	13.6
glioblasto U-118-			Lung ca. (non- sm. cell) HOP-62		
glioblasto SW-783			Lung ca. (non- sm. cell) HOP-62		
neuro*; met SK-N-	17.1	52.5	Lung ca. (non- sm. cell) HOP-62	11.3	3.1

AS			s.cl) NCI-H522		
astrocytoma SF-539	15.5	16.0	Lung ca. (squam.) SW 900	23.2	13.5
astrocytoma SNB-75	43.8	50.0	Lung ca. (squam.) NCI-H596	41.5	10.2
glioma SNB-19	17.9	26.2	Mammary gland	14.8	35.1
glioma U251	47.6	39.0	Breast ca.* (pl.ef) MCF-7	48.6	39.0
glioma SF-295	12.3	10.7	Breast ca.* (pl.ef) MDA-MB-231	25.9	60.7
Heart (fetal)	38.4	8.0	Breast ca.* (pl.ef) T47D	77.4	21.2
Heart	3.5	5.0	Breast ca. BT-549	47.0	95.9
Skeletal muscle (fetal)	17.0	10.0	Breast ca. MDA-N	16.6	7.3
Skeletal muscle	4.4	7.2	Ovary	10.1	4.7
Bone marrow	1.3	14.7	Ovarian ca. OVCAR-3	36.3	31.2
Thymus	13.9	12.3	Ovarian ca. OVCAR-4	33.0	20.7
Spleen	2.6	12.9	Ovarian ca. OVCAR-5	42.6	15.7
Lymph node	1.7	15.9	Ovarian ca. OVCAR-8	8.7	5.2
Colorectal	18.2	11.8	Ovarian ca. IGROV-1	11.3	15.1
Stomach	14.8	33.7	Ovarian ca.* (ascites) SK-OV-3	43.5	17.0
Small intestine	18.3	66.0	Uterus	10.5	21.8
Colon ca. SW480	12.9	14.2	Placenta	2.6	15.0
Colon ca.* SW620(SW480 met)	17.0	14.2	Prostate	11.7	30.6
Colon ca. HT29	17.2	18.8	Prostate ca.* (bone met)PC	35.4	40.3
100.0					
Colon ca. CaCo-2	20.9	7.4	Melanoma	5.0	1.4

			Hs688(A).T		
Colon ca. tissue(ODO3866)	14.7	21.9	Melanoma* (met) Hs688(B).T	6.0	3.5
Colon ca. HCC-2998	22.1	13.1	Melanoma UACC-62	14.3	12.2
Gastric ca.* (liver met) NCI-N87	48.6	82.4	Melanoma M14	3.1	8.2
Bladder	6.2	4.7	Melanoma LOX IMV1	30.1	8.4
Trachea	12.8	49.3	Melanoma* (met) SK-MEL-5	21.8	13.1
Kidney	43.5	35.4	Adipose	9.2	3.0

Table AFE. Panel 2.2

Tissue Name	Rel. Exp.(%) Ag3218, Run 174416494	Tissue Name	Rel. Exp.(%) Ag3218, Run 174416494
Normal Colon	5.9	Kidney Margin (OD04348)	70.2
Colon cancer (OD06064)	5.6	Kidney malignant cancer (OD06204B)	3.9
Colon Margin (OD06064)	3.6	Kidney normal adjacent tissue (OD06204E)	6.7
Colon cancer (OD06159)	6.3	Kidney Cancer (OD04450-01)	15.1
Colon Margin (OD06159)	7.0	Kidney Margin (OD04450-03)	3.1
Colon cancer (OD06297-04)	2.6	Kidney Cancer 8120613	2.5
Colon Margin (OD06297-05)	5.6	Kidney Margin 8120614	18.2
CC Gr.2 ascend colon (ODO3921)	20.0	Kidney Cancer 9010320	2.4
CC Margin (ODO3921)	13.7	Kidney Margin 9010321	4.4
Colon cancer metastasis (OD06104)	0.0	Kidney Cancer 8120607	23.0
Lung Margin	11.0	Kidney Margin	15.1
Lung Margin	0.3	Uterine Cancer 064011	6.1

(OD04451-02)			
Normal Prostate	5.6	Normal Thyroid	6.6
Prostate Cancer (OD04410)	3.9	Thyroid Cancer 064010	6.8
Prostate Margin (OD04410)	6.1	Thyroid Cancer A302152	11.9
Normal Ovary	7.0	Thyroid Margin A302153	7.7
Ovarian cancer (OD06283-03)	1.3	Normal Breast	3.4
Ovarian Margin (OD06283-07)	0.0	Breast Cancer (OD04566)	9.9
Ovarian Cancer 064008	31.2	Breast Cancer 1024	16.8
Ovarian cancer (OD06145)	3.5	Breast Cancer (OD04590-01)	100.0
Ovarian Margin (OD06145)	8.4	Breast Cancer Mets (OD04590-03)	26.2
Ovarian cancer (OD06455-03)	13.7	Breast Cancer Metastasis (OD04655- 05)	36.3
Ovarian Margin (OD06455-07)	1.1	Breast Cancer 064006	5.4
Normal Lung	5.4	Breast Cancer 9100266	12.8
Invasive poor diff. lung adeno (ODO4945-01)	14.5	Breast Margin 9100265	1.0
Lung Margin (ODO4945-03)	2.7	Breast Cancer A209073	3.3
Lung Malignant Cancer (OD03126)	1.8	Breast Margin A2090734	11.7
Lung Margin (OD03126)	5.1	Breast cancer (OD06083)	6.9
Lung Cancer (OD05014A)	12.8	Breast cancer node metastasis (OD06083)	10.7
Lung Margin (OD05014B)	3.3	Normal Liver	9.4
Lung cancer (OD06081)	6.3	Liver Cancer 1026	2.6
Lung Margin (OD06081)	2.7	Liver Cancer 1025	9.7
Lung Cancer (OD04237-01)	12.9	Liver Cancer 6004-T	10.4
Lung Margin	6.1	Liver Tissue 6004-N	5.3
Metastasis			
Ocular Melanoma	0.1	Liver Tissue 6005-N	11.5

Margin (Liver)			
Melanoma Metastasis	1.6	Liver Cancer 064003	22.5
Melanoma Margin (Lung)	4.6	Normal Bladder	6.1
Normal Kidney	10.4	Bladder Cancer 1023	10.8
Kidney Ca, Nuclear grade 2 (OD04338)	14.6	Bladder Cancer A302173	15.1
Kidney Margin (OD04338)	10.5	Normal Stomach	15.0
Kidney Ca Nuclear grade 1/2 (OD04339)	44.8	Gastric Cancer 9060397	7.1
Kidney Margin (OD04339)	17.7	Stomach Margin 9060396	10.4
Kidney Ca, Clear cell type (OD04340)	5.3	Gastric Cancer 9060395	8.4
Kidney Margin (OD04340)	25.3	Stomach Margin 9060394	10.4
Kidney Ca, Nuclear grade 3 (OD04348)	7.5	Gastric Cancer 064005	7.7

Table AFF. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3218, Run 164682519	Rel. Exp.(%) Ag3378, Run 165296553	Tissue Name	Rel. Exp.(%) Ag3218, Run 164682519	Rel. Exp.(%) Ag3378, Run 165296553
Secondary Th1 act	18.2	25.7	HUVEC IL-1beta	14.5	12.9
Secondary Th2 act	39.0	26.6	HUVEC IFN gamma	47.0	25.3
Secondary Tr1 act	33.2	19.1	HUVEC TNF alpha + IFN gamma	43.5	45.1
Secondary Th1 rest	9.5	12.2	HUVEC TNF alpha + IL4	37.1	48.0
Secondary Th2 rest	11.2	5.1	HUVEC IL-11	43.5	18.0
Secondary Tr1 rest	22.7	8.0	Lung Microvascular EC none	16.8	61.6
Primary Th1 act	43.2	27.0	Lung Microvascular EC	18.6	14.7
Primary Th2 act			Lung Microvascular EC		
Primary Tr1 act			Dermal EC none		

Primary Tr1 act	24.7	14.4	Microsvascular Dermal EC TNFalpha + IL- 1beta	66.4	22.1
Primary Th1 rest	25.2	17.4	Bronchial epithelium TNFalpha + IL1beta	30.6	29.3
Primary Th2 rest	15.5	7.5	Small airway epithelium none	36.1	24.3
Primary Tr1 rest	21.3	6.7	Small airway epithelium TNFalpha + IL- 1beta	76.3	62.9
CD45RA CD4 lymphocyte act	35.4	16.6	Coronary artery SMC rest	49.7	28.1
CD45RO CD4 lymphocyte act	27.9	25.9	Coronary artery SMC TNFalpha + IL-1beta	25.3	23.7
CD8 lymphocyte act	21.0	14.8	Astrocytes rest	22.2	31.2
Secondary CD8 lymphocyte rest	39.2	17.8	Astrocytes TNFalpha + IL- 1beta	26.1	25.0
Secondary CD8 lymphocyte act	20.9	7.4	KU-812 (Basophil) rest	90.8	85.3
CD4 lymphocyte none	4.5	11.8	KU-812 (Basophil) PMA/ionomycin	87.1	72.2
2ry Th1/Th2/Tr1 _anti- CD95 CH11	2.6	10.0	CCD1106 (Keratinocytes) none	36.6	36.9
LAK cells rest	11.7	12.3	CCD1106 (Keratinocytes) TNFalpha + IL- 1beta	33.4	20.4
LAK cells IL-2	6.8	27.5	Liver cirrhosis	25.5	19.9
LAK cells IL-2+IL- 12	37.1	11.6	Lupus kidney	44.4	15.7
LAK cells IL- 2+IFN gamma	20.7	19.1	NCI-H292 none	79.6	64.6
LAK cells IL-2+ IFN gamma	21.9	14.7	NCI-H292 IL-4	85.3	96.6
NK Cells IL-2 rest	11.9	11.7	NCI-H292 IL-12	98.8	29.1
Two Way MLR 3	23.7	11.0	NCI-H292 IFN	80.1	56.6

day			gamma		
Two Way MLR 5 day	12.5	6.1	HPAEC none	38.4	27.2
Two Way MLR 7 day	12.3	8.7	HPAEC TNF alpha + IL-1 beta	42.6	43.2
PBMC rest	6.0	5.7	Lung fibroblast none	31.2	21.3
PBMC PWM	40.3	27.7	Lung fibroblast TNF alpha + IL-1 beta	14.7	24.5
PBMC PHA-L	37.9	17.7	Lung fibroblast IL-4	47.0	42.6
Ramos (B cell) none	11.7	14.9	Lung fibroblast IL-9	49.3	30.6
Ramos (B cell) ionomycin	33.9	26.8	Lung fibroblast IL-13	36.6	42.6
B lymphocytes PWM	33.7	40.9	Lung fibroblast IFN gamma	44.8	22.5
B lymphocytes CD40L and IL-4	34.4	18.3	Dermal fibroblast CCD1070 rest	33.7	47.3
EOL-1 dbcAMP	50.0	28.1	Dermal fibroblast CCD1070 TNF alpha	47.3	33.2
EOL-1 dbcAMP PMA/ionomycin	44.1	32.1	Dermal fibroblast CCD1070 IL-1 beta	50.0	34.6
Dendritic cells none	33.9	19.6	Dermal fibroblast IFN gamma	24.0	34.4
Dendritic cells LPS	21.9	10.2	Dermal fibroblast IL-4	24.3	32.8
Dendritic cells anti-CD40	49.7	33.9	IBD Colitis 2	6.0	11.7
Monocytes rest	10.7	10.3	IBD Crohn's	25.3	26.1
Monocytes LPS	30.6	9.3	Colon	70.7	100.0
Macrophages rest	41.2	33.7	Lung	64.6	17.7
Macrophages LPS	20.0	7.5	Thymus	80.7	56.3
HUVEC none	26.8	29.5	Kidney	26.4	41.5
HUVEC starved	26.2	37.6			

CNS_neurodegeneration_v1.0 Summary: Ag3218/Ag3378 - Two different experiments using probe/primer sets with the same sequence are in very good agreement. This panel

dependent group of individuals. The Ag3218 and Ag3378 potential expression of the 2017 was detected between Alzheimer's diseased postmortem brains and those of non-demented controls

in this experiment. Please see Panel 1.3D for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

Panel 1.3D Summary: Ag3218/Ag3378 - Two different experiments using probe/primer sets with the same sequence are in good agreement. Highest expression is seen in testis and a lung cancer cell line (CTs=30-31). This panel confirms the expression of this gene at low levels in the brain. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

This gene product is also expressed in adipose, pancreas, thyroid, pituitary, heart, and liver. This widespread expression in tissues with metabolic function suggests that this gene product may be important for the pathogenesis, diagnosis, and/or treatment of metabolic and endocrine diseases, including obesity and Types 1 and 2 diabetes.

Based on expression in this panel, this gene may be involved in gastric, pancreatic, brain, colon, renal, lung, breast, ovarian and prostate cancer as well as melanomas. Thus, expression of this gene could be used as a diagnostic marker for the presence of these cancers. Furthermore, therapeutic inhibition using antibodies or small molecule drugs might be of use in the treatment of these cancers.

Panel 2.2 Summary: Ag3218 - This gene is expressed at low to moderate levels in many samples on this panel, with the highest levels of expression in breast cancer sample OD04590-01 (CT=30.3). This gene is expressed in a cluster of breast cancer samples with no expression in normal breast (CT>35). Similarly, this gene is expressed in ovarian cancer samples at higher levels than the matched margin samples.

Interestingly, this gene is expressed at higher levels in kidney cancer margin samples than in the matched cancer samples.

This gene is homologous to a mouse myosin phosphatase targeting subunit (MYPT) which have been found to play a role in cell division. MYPT undergoes mitosis-specific phosphorylation which is reversed during cytokinesis.

SEQUENCE

1. Totsukawa G, Yamakita Y, Yamashiro S, Hosoya H, Hartshorne DJ, Matsumura F. Activation of myosin phosphatase targeting subunit by mitosis-specific phosphorylation. J Cell Biol 1999 Feb 22;144(4):735-44.

Panel 4D Summary: Ag3218/Ag3378 - Two different experiments using probe/primer sets with the same sequence are in very good agreement. Highest expression is seen in the colon and a mucoepidermoid cell line (CTs=30-32). This gene is expressed at low to moderate levels in a wide range of cell types of significance in the immune response in health and disease. These cells include members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

AG. CG59241-01: Amiloride-sensitive sodium channel

Expression of gene CG59241-01 was assessed using the primer-probe set Ag3407, described in Table AGA. Results of the RTQ-PCR runs are shown in Tables AGB, AGC and AGD.

Table AGA. Probe Name Ag3407

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtcacccctctgcaacactaatg-3'	22	268	496
Probe	TET-5'-ctgtcccagctcagctaccctgactt-3'-TAMRA	26	298	497
Reverse	5'-tttcatccagtcaccagcat-3'	19	340	498

Table AGB. CNS neurodegeneration x1.0

Tissue Name	Rel. Exp. of Ag3407 Run 210349883	Tissue Name	Rel. Exp. of Ag3407 Run 210349883
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AD 1 Hippo	18.4	Control (Path) 3 Temporal Ctx	4.1
AD 2 Hippo	29.7	Control (Path) 4 Temporal Ctx	40.3
AD 3 Hippo	18.3	AD 1 Occipital Ctx	36.9
AD 4 Hippo	5.4	AD 2 Occipital Ctx (Missing)	0.0
AD 5 hippo	91.4	AD 3 Occipital Ctx	19.1
AD 6 Hippo	80.7	AD 4 Occipital Ctx	18.8
Control 2 Hippo	9.3	AD 5 Occipital Ctx	18.3
Control 4 Hippo	19.9	AD 6 Occipital Ctx	28.9
Control (Path) 3 Hippo	8.8	Control 1 Occipital Ctx	4.3
AD 1 Temporal Ctx	28.5	Control 2 Occipital Ctx	80.1
AD 2 Temporal Ctx	41.8	Control 3 Occipital Ctx	20.2
AD 3 Temporal Ctx	32.5	Control 4 Occipital Ctx	6.0
AD 4 Temporal Ctx	36.3	Control (Path) 1 Occipital Ctx	92.7
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	25.3
AD 5 Sup Temporal Ctx	56.6	Control (Path) 3 Occipital Ctx	3.0
AD 6 Inf Temporal Ctx	82.4	Control (Path) 4 Occipital Ctx	41.2
AD 6 Sup Temporal Ctx	44.1	Control 1 Parietal Ctx	21.9
Control 1 Temporal Ctx	15.3	Control 2 Parietal Ctx	79.0
Control 2 Temporal Ctx	24.1	Control 3 Parietal Ctx	22.2
Control 3 Temporal Ctx	34.6	Control (Path) 1 Parietal Ctx	77.9
Control 4 Temporal Ctx	12.0	Control (Path) 2 Parietal Ctx	47.6
Control (Path) 1 Temporal Ctx	53.6	Control (Path) 3 Parietal Ctx	6.2
Control (Path) 2 Temporal Ctx	56.6	Control (Path) 4 Parietal Ctx	67.4

Tissue Name	Rel. Exp.(%) Ag3407,	Tissue Name	Rel. Exp.(%) Ag3407,
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	Run 216821458		Run 216821458
Adipose	0.2	Renal ca. TK-10	16.6
Melanoma* Hs688(A).T	2.3	Bladder	0.3
Melanoma* Hs688(B).T	0.4	Gastric ca. (liver met.) NCI-N87	8.8
Melanoma* M14	2.0	Gastric ca. KATO III	0.7
Melanoma* LOXIMVI	2.5	Colon ca. SW-948	3.7
Melanoma* SK- MEL-5	8.7	Colon ca. SW480	14.1
Squamous cell carcinoma SCC-4	1.2	Colon ca.* (SW480 met) SW620	21.2
Testis Pool	0.4	Colon ca. HT29	10.7
Prostate ca.* (bone met) PC-3	4.4	Colon ca. HCT-116	64.2
Prostate Pool	2.3	Colon ca. CaCo-2	32.3
Placenta	0.5	Colon cancer tissue	13.2
Uterus Pool	0.0	Colon ca. SW1116	12.5
Ovarian ca. OVCAR-3	8.4	Colon ca. Colo-205	0.3
Ovarian ca. SK-OV- 3	9.7	Colon ca. SW-48	0.6
Ovarian ca. OVCAR-4	1.6	Colon Pool	2.8
Ovarian ca. OVCAR-5	18.9	Small Intestine Pool	4.5
Ovarian ca. IGROV- 1	4.9	Stomach Pool	1.4
Ovarian ca. OVCAR-8	5.9	Bone Marrow Pool	1.8
Ovary	2.0	Fetal Heart	2.4
Breast ca. MCF-7	16.7	Heart Pool	0.3
Breast ca. MDA- MB-231	12.1	Lymph Node Pool	3.5
Breast ca. BT 549	22.7	Fetal Skeletal Muscle	1.9
Breast ca. T47D	27.4	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	4.5	Spleen Pool	0.0
Breast Pool	2.9	Thymus Pool	2.1
T. B.S.	0.0	CNS cancer (glio/astro)	0.0
T. S. M.C.			
Fetal Lung	10.8	CNS cancer	58.6

		(neuro;met) SK-N-AS	
Lung ca. NCI-N417	1.3	CNS cancer (astro) SF-539	28.1
Lung ca. LX-1	21.8	CNS cancer (astro) SNB-75	24.7
Lung ca. NCI-H146	5.4	CNS cancer (glio) SNB-19	7.3
Lung ca. SHP-77	11.7	CNS cancer (glio) SF-295	4.8
Lung ca. A549	8.0	Brain (Amygdala) Pool	3.9
Lung ca. NCI-H526	0.0	Brain (cerebellum)	36.1
Lung ca. NCI-H23	7.4	Brain (fetal)	100.0
Lung ca. NCI-H460	5.4	Brain (Hippocampus) Pool	5.6
Lung ca. HOP-62	2.9	Cerebral Cortex Pool	5.6
Lung ca. NCI-H522	8.5	Brain (Substantia nigra) Pool	7.1
Liver	0.0	Brain (Thalamus) Pool	11.3
Fetal Liver	0.0	Brain (whole)	13.4
Liver ca. HepG2	0.8	Spinal Cord Pool	12.7
Kidney Pool	2.1	Adrenal Gland	0.0
Fetal Kidney	3.7	Pituitary gland Pool	0.0
Renal ca. 786-0	1.7	Salivary Gland	0.9
Renal ca. A498	0.7	Thyroid (female)	0.0
Renal ca. ACHN	1.9	Pancreatic ca. CAPAN2	2.3
Renal ca. UO-31	0.2	Pancreas Pool	2.6

Table AGD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3407, Run 165296462	Tissue Name	Rel. Exp.(%) Ag3407, Run 165296462
Secondary Th1 act	7.9	HUVEC IL-1beta	0.0
Secondary Th2 act	17.1	HUVEC IFN gamma	0.0
Secondary Tr1 act	40.1	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	4.4	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	7.0	HUVEC IL-11	0.0
Secondary Tr1 rest	11.7	Lung Microvascular EC	0.0
Primary Th2 act	69.3	Microvascular Dermal EC	0.0
		none	

Primary Tr1 act	90.8	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	20.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	42.6	Small airway epithelium none	3.0
Primary Tr1 rest	52.5	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	2.8	Coronary artery SMC rest	3.6
CD45RO CD4 lymphocyte act	14.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	5.8	Astrocytes rest	11.6
Secondary CD8 lymphocyte rest	18.9	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	22.2	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti- CD95 CH11	4.5	CCD1106 (Keratinocytes) none	2.7
LAK cells rest	3.3	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	4.0	Liver cirrhosis	13.5
LAK cells IL-2+IL-12	5.7	Lupus kidney	4.1
LAK cells IL-2+IFN gamma	21.3	NCI-H292 none	9.0
LAK cells IL-2+ IL-18	6.7	NCI-H292 IL-4	14.8
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	3.5
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	5.0	NCI-H292 IFN gamma	5.5
Two Way MLR 5 day	2.3	HPAEC none	0.0
Two Way MLR 7 day	8.2	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	2.8
PBMC PWM	21.3	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	20.4	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0

B lymphocytes PWM	100.0	Human fibroblast IL-1 gamma	0.0
B lymphocytes CD40L	19.8	Dermal fibroblast	34.4

and IL-4		CCD1070 rest	
EOL-1 dbcAMP	2.6	Dermal fibroblast CCD1070 TNF alpha	68.8
EOL-1 dbcAMP PMA/ionomycin	6.2	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	14.1
Dendritic cells anti- CD40	6.0	IBD Colitis 2	0.0
Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	6.5	Colon	42.3
Macrophages rest	0.0	Lung	35.8
Macrophages LPS	0.0	Thymus	45.4
HUVEC none	0.0	Kidney	55.1
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3407 This panel confirms the expression of this gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3407 Highest expression of the CG59241-01 gene is seen in fetal brain (CT=31.3). Furthermore, low to moderate levels of expression is also observed in CNS cancer cell lines (CTs=32-34). The CG59241-01 gene codes for a putative amiloride-sensitive sodium channel. A similar amiloride-sensitive sodium channel was shown to be highly expressed in malignant glioblastoma multiforme tumors and to be a characteristic feature of malignant brain tumor cells (Ref.1). Therefore, therapeutic modulation of the activity of the protein encoded by this gene may be beneficial in the treatment of CNS cancer. Significant expression is also seen in a cluster of cell lines derived from brain, colon, breast, and ovarian cancers. Therefore, therapeutic modulation of the activity of this gene or its protein product, through the use of small molecule drugs, protein therapeutics or antibodies, might be beneficial in the treatment of these cancers.

cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system

disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

References:

1. Bubien JK, Keeton DA, Fuller CM, Gillespie GY, Reddy AT, Mapstone TB, Benos DJ. (1999) Malignant human gliomas express an amiloride-sensitive Na⁺ conductance. *Am J Physiol* 276(6 Pt 1):C1405-10

Panel 4D Summary: Ag3407 Highest expression Of the CG59241-01 gene is detected in PWM treated B lymphocytes (CT=32). Similar expression is also detected in primary activated Th1, Th2 and Tr1 cells, as well as TNF alpha treated dermal fibroblast CCD1070 cells (CTs=32). Therefore, expression of this gene can be used to distinguish these samples from other samples in the panel. Furthermore, this gene is expressed in activated lymphocytes. Likewise, no expression of this gene is seen in PBMC that contain normal B cells (CT=40), but it is induced when PBMC are treated with the pokeweed mitogen or PHA-L (CTs=34). In addition, the transcript is not seen in the B cell lymphoma Ramos regardless of stimulation. Therefore, the gene product could potentially be used therapeutically in the treatment of Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, lupus erythematosus, psoriasis and in other diseases in which T cells and B cells are activated.

In addition, low expression of this gene is also observed in normal colon, lung, thymus and kidney tissues. The CG59241-01 gene encodes an amiloride-sensitive sodium channel. A similar channel, the amiloride-sensitive epithelial sodium channel (ENaC) constitutes the limiting step for sodium reabsorption in epithelial cells that line the distal nephron, distal colon, ducts of several exocrine glands and lung airways and plays an important role in pathophysiological and clinical conditions such as hypertension or lung edema. ENaC has been implicated in two genetic diseases, Liddle's syndrome and pseudohypoaldosteronism (PHA-1) (Ref.1). Therefore, antibody or small molecule therapies designed with the protein encoded for by CG59241-01 gene could modulate kidney/colon/lung function and be important in the treatment of inflammatory or autoimmune diseases of these tissues in addition

Reference:

1. Hummler E. (1998) Reversal of convention: from man to experimental animal in elucidating the function of the renal amiloride-sensitive sodium channel. Exp Nephrol 1998 Jul-Aug;6(4):265-71

AH. CG58602-01: FAD binding domain containing protein

Expression of gene CG58602-01 was assessed using the primer-probe set Ag3385, described in Table AHA. Results of the RTQ-PCR runs are shown in Tables AHB, AHC and AHD.

Table AHA. Probe Name Ag3385

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tcatgaatccaggcaaagtg-3'	20	1427	499
Probe	TET-5'-ttagcccacaagttccctgactacgg-3'- TAMRA	26	1468	500
Reverse	5'-tgggcatgaagaaaagttcca-3'	20	1503	501

Table AHB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3385, Run 210154892	Tissue Name	Rel. Exp.(%) Ag3385, Run 210154892
AD 1 Hippo	34.6	Control (Path) 3 Temporal Ctx	21.2
AD 2 Hippo	47.6	Control (Path) 4 Temporal Ctx	36.1
AD 3 Hippo	11.9	AD 1 Occipital Ctx	28.1
AD 4 Hippo	24.3	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	56.3	AD 3 Occipital Ctx	15.0
AD 6 Hippo	63.3	AD 4 Occipital Ctx	34.9
Control 2 Hippo	42.6	AD 5 Occipital Ctx	52.1
Control 4 Hippo	24.7	AD 6 Occipital Ctx	25.3
Control (Path) 3 Hippo	23.3	Control 1 Occipital Ctx	14.3
AD 1 Temporal Ctx	23.8	Control 2 Occipital Ctx	69.3
		Control 3 Occipital Ctx	
AD 4 Temporal Ctx	39.0	Control (Path) 1	68.3

		Occipital Ctx	
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	11.0
AD 5 Sup Temporal Ctx	55.5	Control (Path) 3 Occipital Ctx	8.9
AD 6 Inf Temporal Ctx	64.2	Control (Path) 4 Occipital Ctx	17.3
AD 6 Sup Temporal Ctx	54.0	Control 1 Parietal Ctx	32.8
Control 1 Temporal Ctx	23.8	Control 2 Parietal Ctx	62.0
Control 2 Temporal Ctx	50.3	Control 3 Parietal Ctx	33.4
Control 3 Temporal Ctx	38.4	Control (Path) 1 Parietal Ctx	70.7
Control 3 Temporal Ctx	19.2	Control (Path) 2 Parietal Ctx	31.4
Control (Path) 1 Temporal Ctx	56.6	Control (Path) 3 Parietal Ctx	20.9
Control (Path) 2 Temporal Ctx	47.6	Control (Path) 4 Parietal Ctx	43.2

Table AHC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3385, Run 217043538	Tissue Name	Rel. Exp.(%) Ag3385, Run 217043538
Adipose	2.4	Renal ca. TK-10	3.5
Melanoma* Hs688(A).T	0.7	Bladder	6.6
Melanoma* Hs688(B).T	1.1	Gastric ca. (liver met.) NCI-N87	2.1
Melanoma* M14	0.9	Gastric ca. KATO III	0.9
Melanoma* LOXIMVI	1.3	Colon ca. SW-948	4.5
Melanoma* SK-MEL-5	2.2	Colon ca. SW480	0.8
Squamous cell carcinoma SCC-4	0.1	Colon ca.* (SW480 met) SW620	1.3
Testis Pool	1.3	Colon ca. HT29	0.6
Prostate ca.* (bone met) PC-3	5.8	Colon ca. HCT-116	1.9
Uterus Pool	0.2	Colon ca. SW1116	0.9
Ovarian ca.	1.1	Colon ca. Colo-205	3.5

OVCAR-3			
Ovarian ca. SK-OV-3	3.7	Colon ca. SW-48	4.2
Ovarian ca. OVCAR-4	0.2	Colon Pool	3.0
Ovarian ca. OVCAR-5	42.0	Small Intestine Pool	3.5
Ovarian ca. IGROV-1	8.0	Stomach Pool	1.8
Ovarian ca. OVCAR-8	2.7	Bone Marrow Pool	0.9
Ovary	3.3	Fetal Heart	12.9
Breast ca. MCF-7	10.3	Heart Pool	8.3
Breast ca. MDA-MB-231	3.0	Lymph Node Pool	3.5
Breast ca. BT 549	1.3	Fetal Skeletal Muscle	2.6
Breast ca. T47D	100.0	Skeletal Muscle Pool	25.5
Breast ca. MDA-N	0.4	Spleen Pool	0.2
Breast Pool	3.1	Thymus Pool	2.7
Trachea	3.2	CNS cancer (glio/astro) U87-MG	4.0
Lung	2.9	CNS cancer (glio/astro) U-118-MG	1.3
Fetal Lung	3.0	CNS cancer (neuro;met) SK-N-AS	1.8
Lung ca. NCI-N417	0.2	CNS cancer (astro) SF-539	1.3
Lung ca. LX-1	1.1	CNS cancer (astro) SNB-75	0.9
Lung ca. NCI-H146	0.4	CNS cancer (glio) SNB-19	5.0
Lung ca. SHP-77	3.1	CNS cancer (glio) SF-295	5.5
Lung ca. A549	4.3	Brain (Amygdala) Pool	5.5
Lung ca. NCI-H526	0.4	Brain (cerebellum)	13.5
Lung ca. NCI-H23	6.8	Brain (fetal)	5.6
Lung ca. NCI-H460	1.5	Brain (Hippocampus) Pool	5.2
Lung ca. HOP-62	0.1	Cerebral Cortex Pool	7.1
Lung ca. NCI-H522	3.6	Brain (Substantia nigra)	11.5
Liver ca. HepG2	2.7	Spinal Cord Pool	4.8

Kidney Pool	6.2	Adrenal Gland	6.0
Fetal Kidney	4.0	Pituitary gland Pool	1.7
Renal ca. 786-0	0.2	Salivary Gland	6.6
Renal ca. A498	1.4	Thyroid (female)	5.2
Renal ca. ACHN	0.8	Pancreatic ca. CAPAN2	3.5
Renal ca. UO-31	0.9	Pancreatic Pool	4.4

Table AHD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3385, Run 165296471	Tissue Name	Rel. Exp.(%) Ag3385, Run 165296471
Secondary Th1 act	1.2	HUVEC IL-1beta	0.0
Secondary Th2 act	3.6	HUVEC IFN gamma	3.7
Secondary Tr1 act	2.6	HUVEC TNF alpha + IFN gamma	0.7
Secondary Th1 rest	0.4	HUVEC TNF alpha + IL4	2.2
Secondary Th2 rest	0.9	HUVEC IL-11	1.3
Secondary Tr1 rest	0.4	Lung Microvascular EC none	3.2
Primary Th1 act	1.1	Lung Microvascular EC TNFalpha + IL-1beta	1.5
Primary Th2 act	0.7	Microvascular Dermal EC none	3.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	1.1	Bronchial epithelium TNFalpha + IL1beta	0.6
Primary Th2 rest	0.5	Small airway epithelium none	0.7
Primary Tr1 rest	0.6	Small airway epithelium TNFalpha + IL-1beta	0.8
CD45RA CD4 lymphocyte act	2.0	Coronary artery SMC rest	0.5
CD45RO CD4 lymphocyte act	3.7	Coronary artery SMC TNFalpha + IL-1beta	2.0
CD8 lymphocyte act	0.9	Astrocytes rest	1.5
Secondary CD8 lymphocyte rest	2.7	Astrocytes TNFalpha + IL-1beta	2.6
Secondary CD8	0.0	KU-812 (Basophil) rest	3.0
Secondary Th1 Th2 Tr1 anti-	0.0	CCD1106 (Keratinocytes)	3.3

CD95 CH11		none	
LAK cells rest	9.4	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.3
LAK cells IL-2	0.8	Liver cirrhosis	7.9
LAK cells IL-2+IL-12	1.5	Lupus kidney	2.3
LAK cells IL-2+IFN gamma	3.7	NCI-H292 none	3.3
LAK cells IL-2+ IL-18	2.5	NCI-H292 IL-4	8.4
LAK cells PMA/ionomycin	2.0	NCI-H292 IL-9	2.6
NK Cells IL-2 rest	0.7	NCI-H292 IL-13	2.9
Two Way MLR 3 day	4.6	NCI-H292 IFN gamma	1.8
Two Way MLR 5 day	2.8	HPAEC none	2.3
Two Way MLR 7 day	1.8	HPAEC TNF alpha + IL-1 beta	1.9
PBMC rest	0.6	Lung fibroblast none	1.5
PBMC PWM	11.0	Lung fibroblast TNF alpha + IL-1 beta	0.7
PBMC PHA-L	2.3	Lung fibroblast IL-4	1.6
Ramos (B cell) none	0.0	Lung fibroblast IL-9	2.0
Ramos (B cell) ionomycin	0.9	Lung fibroblast IL-13	0.9
B lymphocytes PWM	3.5	Lung fibroblast IFN gamma	0.7
B lymphocytes CD40L and IL-4	5.4	Dermal fibroblast CCD1070 rest	1.6
EOL-1 dbcAMP	5.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	1.2	Dermal fibroblast CCD1070 IL-1 beta	2.3
Dendritic cells none	15.5	Dermal fibroblast IFN gamma	0.5
Dendritic cells LPS	4.5	Dermal fibroblast IL-4	0.4
Dendritic cells anti- CD40	11.7	IBD Colitis 2	0.3
Monocytes rest	8.7	IBD Crohn's	0.0
Monocytes LPS	0.6	Colon	5.1
Macrophages rest	13.5	Lung	6.7
Macrophages LPS	1.6	Thymus	100.0
HUVEC none	0.6	Kidney	11.3

CGNS_neurodegeneration_v1.0 Summary: August 2002 This panel confirms the expression of the CG58602-01 gene at low levels in the brains of an independent group of individuals.

However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3385 Highest expression of the CG58602-01 gene is seen in a breast cancer cell line (CT=26.3). Significant expression is also seen in an ovarian cancer cell line. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of breast and ovarian cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of breast and ovarian cancers.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

Expression of this gene is higher in fetal skeletal muscle (CT=28.3) when compared to expression in adult skeletal muscle (CT=31.5). Thus, expression of this gene could be used to distinguish fetal from adult skeletal muscle.

In addition, this gene is expressed at high levels (CTs=29-30.4) in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

Panel 4D Summary: Ag3385 Highest expression of the CG58602-01 gene is seen in the thymus (CT=28). Thus, the putative protein encoded for by this gene could therefore play an important role in T cell development. Therefore, small molecule therapeutics designed against

AI. CG58468-01: Serum Amyloid P Component

Expression of gene CG58468-01 was assessed using the primer-probe set Ag3356, described in Table AIA. Results of the RTQ-PCR runs are shown in Table AIB.

Table AIA. Probe Name Ag3356

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' - aggcatttattttccctcaaga - 3'	22	106	502
Probe	TET-5' - agtctatgtgtccctgatccccaagg - 3' - TAMRA	26	137	503
Reverse	5' - gttttcaggcaaagcttgaagt - 3'	22	181	504

Table AIB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3356, Run 216523476	Tissue Name	Rel. Exp.(%) Ag3356, Run 216523476
Adipose	2.2	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK-MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	1.7	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0

Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	10.7
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	2.6
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	25.9
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	2.1
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	19.6	Thymus Pool	0.0
Trachea	1.5	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	5.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	38.7	Brain (fetal)	2.6
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	2.3	Brain (Thalamus) Pool	0.0
Fetal Liver	0.0	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	2.1
Kidney Pool	19.1	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	2.1
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

CNS_neurodegeneration_v1.0 Summary: Ag3356 Expression of the CG58468-01 gene is low/undetectable in all the samples on this panel. (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3356 Expression of the CG58468-01 gene is restricted to the colon (CT=34). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel.

Panel 4D Summary: Ag3356 Results from one experiment with the CG56003-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

AJ. CG58183-01: N-METHYL-D-ASPARTATE RECEPTOR

Expression of gene CG58183-01 was assessed using the primer-probe set Ag3355, described in Table AJA. Results of the RTQ-PCR runs are shown in Tables AJB, AJC and AJD.

Table AJA. Probc Name Ag3355

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gctggccaactctgtctagac-3'	21	1617	505
Probe	TET-5'-tgactcttccacattggacagccttt-3'-TAMRA	26	1649	506
Reverse	5'-ttactgctatggaggctgctaa-3'	22	1675	507

Table AJB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3355, Run 210142850	Tissue Name	Rel. Exp.(%) Ag3355, Run 210142850
AD 1 Hippo	17.7	Control (Path) 3 Temporal Ctx	7.3
AD 2 Hippo	27.4	Control (Path) 4 Temporal Ctx	47.6
AD 3 Hippo	8.8	AD 1 Occipital Ctx	18.8
AD 4 Hippo	16.2	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	53.6	AD 3 Occipital Ctx	3.0
AD 6 Hippo	51.4	AD 4 Occipital Ctx	27.2
Control 3 Hippo	4.5	Control 1 Occipital Ctx	2.8

AD 1 Temporal Ctx	18.3	Control 2 Occipital Ctx	39.0
AD 2 Temporal Ctx	48.0	Control 3 Occipital Ctx	18.2
AD 3 Temporal Ctx	5.7	Control 4 Occipital Ctx	3.4
AD 4 Temporal Ctx	15.2	Control (Path) 1 Occipital Ctx	81.8
AD 5 Inf Temporal Ctx	61.6	Control (Path) 2 Occipital Ctx	9.0
AD 5 Sup Temporal Ctx	69.3	Control (Path) 3 Occipital Ctx	0.0
AD 6 Inf Temporal Ctx	66.9	Control (Path) 4 Occipital Ctx	13.3
AD 6 Sup Temporal Ctx	62.9	Control 1 Parietal Ctx	6.6
Control 1 Temporal Ctx	8.5	Control 2 Parietal Ctx	74.7
Control 2 Temporal Ctx	66.9	Control 3 Parietal Ctx	21.0
Control 3 Temporal Ctx	34.9	Control (Path) 1 Parietal Ctx	100.0
Control 3 Temporal Ctx	7.0	Control (Path) 2 Parietal Ctx	21.9
Control (Path) 1 Temporal Ctx	90.1	Control (Path) 3 Parietal Ctx	6.0
Control (Path) 2 Temporal Ctx	74.7	Control (Path) 4 Parietal Ctx	50.7

Table AJC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3355, Run 216523475	Tissue Name	Rel. Exp.(%) Ag3355, Run 216523475
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.9	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca. * (SW45) (met) SW620	0.0

Testis Pool	2.4	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	2.1	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.3	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	2.2
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	3.4
Ovarian ca. IGROV-1	0.0	Stomach Pool	2.4
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	1.5
Ovary	4.4	Fetal Heart	1.9
Breast ca. MCF-7	0.0	Heart Pool	3.6
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	2.9
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	1.8
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	4.3
Breast Pool	5.7	Thymus Pool	4.7
Trachea	1.7	CNS cancer (glio/astro) U87-MG	0.0
Lung	1.6	CNS cancer (glio/astro) U-118-MG	0.1
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	3.2
Lung ca. NCI-N417	17.8	CNS cancer (astro) SF-539	14.8
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	17.6
Lung ca. NCI-H146	4.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	11.7	CNS cancer (glio) SF-295	0.0
Brain (Hippocampus)			
Lung ca. NCI-H2079	0.0	Brain (Hippocampus)	0.0
Lung ca. NCI-H460	0.3	Brain (Hippocampus)	33.0

		Pool	
Lung ca. HOP-62	0.3	Cerebral Cortex Pool	42.3
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	43.8
Liver	0.2	Brain (Thalamus) Pool	50.7
Fetal Liver	0.4	Brain (whole)	71.2
Liver ca. HepG2	0.0	Spinal Cord Pool	15.0
Kidney Pool	1.4	Adrenal Gland	0.0
Fetal Kidney	7.2	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.1
Renal ca. A498	0.0	Thyroid (female)	0.1
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	2.7

Table AJD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3355, Run 165241988	Tissue Name	Rel. Exp.(%) Ag3355, Run 165241988
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	11.8	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4			
lymphocyte act		TNFalpha + IL-1beta	
CD8 lymphocyte act	0.0	Astrocytes rest	0.0

Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	57.8
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	67.4
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	39.8
LAK cells IL-2+IL-12	0.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Monocytes rest	0.0	Dendritic cells	0.0
Monocytes LPS	0.0	Colon	12.7

Macrophages rest	0.0	Lung	15.2
Macrophages LPS	0.0	Thymus	100.0
HUVEC none	0.0	Kidney	73.2
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3355 This panel confirms the expression of CG58183-01 gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3355 Highest expression of CG58183-01 gene is detected in fetal brain (Ct=29.2). In addition, this gene is expressed at high levels in all regions of the central nervous system examined, including amygdala, hippocampus, substantia nigra, thalamus, cerebellum, cerebral cortex, and spinal cord (CTs= 29-32). Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

This gene codes for N-methyl-D-aspartate (NMDA) receptor 3A protein. In cats and rodent models competitive NMDA receptor antagonists, such as D-(E)-4-(3-phosphonoprop-2-enyl)piperazine-2-carboxylic acid, which act at the neurotransmitter recognition site were shown to be effective in reducing ischaemic brain damage when administered prior to the onset of an ischaemic episode (Ref. 1). Therefore, therapeutic modulation of the activity of the protein encoded by this gene may be beneficial in the treatment of ischaemic brain.

Among tissues with metabolic or endocrine function, this gene is expressed at low levels in pancreas, heart, and the gastrointestinal tract. Therefore, therapeutic modulation of the activity of this gene may prove useful in the treatment of endocrine/metabolically related diseases, such as obesity and diabetes.

Furthermore, low to moderate expression of this gene is detected in lung cancer, and CNS cancer cell lines. Therefore, therapeutic modulation of the activity of this gene or its

References:

1. McCulloch J. (1991) Ischaemic brain damage--prevention with competitive and non-competitive antagonists of N-methyl-D-aspartate receptors. *Arzneimittelforschung* 41(3A):319-24.

Panel 4D Summary: Ag3355 Expression of the CG58183-01 gene is limited to a few samples, with highest expression in the thymus (CT=33.5). Thus, expression of this gene may be useful as a marker of thymic tissue. Low, but significant levels of expression are also seen in the kidney, in TNF-alpha and IL-1 beta treated astrocytes and in the PMA/ionomycin treated basophil cell line KU-812. Thus, this gene product may be involved in the normal homeostasis of this tissue. Therefore, agonistic antibodies or protein therapeutics may be important in the treatment of inflammatory or autoimmune diseases that affect the kidney, including lupus and glomerulonephritis. In addition, the expression of this transcript in astrocytes treated with TNF-a and IL-1 indicates that therapeutics designed against the protein encoded by this gene may be useful for the treatment of inflammatory CNS diseases such as multiple sclerosis.

AK. CG59315-01: connexin

Expression of gene CG59315-01 was assessed using the primer-probe set Ag3542, described in Table AKA. Results of the RTQ-PCR runs are shown in Tables AKB and AKC.

Table AKA. Probe Name Ag3542

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ggacacctcccaacctagatc-3'	21	1024	508
Probe	TET-5'-tacctgtcttccttccttgaggctgg-3'- TAMRA	26	1046	509
Reverse	5'-ttgcattcttgtgtccatgag-3'	21	1081	510

Table AKB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3542, Run 217049297	Tissue Name	Rel. Exp.(%) Ag3542, Run 217049297
Adipose	17.3	Renal ca. TK-10	6.8
Melanoma*			
Hs088(B).1		NCL-N8	
Melanoma* M14	12.2	Gastric ca. KATO III	12.2

Melanoma* LOXIMVI	0.0	Colon ca. SW-948	3.8
Melanoma* SK- MEL-5	0.7	Colon ca. SW480	39.0
Squamous cell carcinoma SCC-4	2.0	Colon ca.* (SW480 met) SW620	6.7
Testis Pool	0.3	Colon ca. HT29	2.3
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	17.7
Prostate Pool	0.0	Colon ca. CaCo-2	2.8
Placenta	1.2	Colon cancer tissue	1.6
Uterus Pool	0.0	Colon ca. SW1116	0.3
Ovarian ca. OVCAR-3	6.3	Colon ca. Colo-205	0.3
Ovarian ca. SK-OV- 3	2.5	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	1.7
Ovarian ca. OVCAR-5	25.0	Small Intestine Pool	6.3
Ovarian ca. IGROV- 1	6.4	Stomach Pool	5.4
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	3.1
Ovary	0.6	Fetal Heart	1.7
Breast ca. MCF-7	12.9	Heart Pool	1.5
Breast ca. MDA- MB-231	5.0	Lymph Node Pool	3.6
Breast ca. BT 549	8.7	Fetal Skeletal Muscle	0.0
Breast ca. T47D	100.0	Skeletal Muscle Pool	6.1
Breast ca. MDA-N	2.7	Spleen Pool	5.8
Breast Pool	4.9	Thymus Pool	3.0
Trachea	9.3	CNS cancer (glio/astro) U87-MG	1.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	13.7
Fetal Lung	3.2	CNS cancer (neuro;met) SK-N-AS	35.4
Lung ca. NCI-N417	1.2	CNS cancer (astro) SF- 539	4.9
Lung ca. NCI-H146		CNS cancer (astro) SNB-19	
Lung ca. SHP-77	8.1	CNS cancer (glio) SF-	12.5

		295	
Lung ca. A549	10.8	Brain (Amygdala) Pool	0.4
Lung ca. NCI-H526	2.1	Brain (cerebellum)	13.6
Lung ca. NCI-H23	8.1	Brain (fetal)	6.9
Lung ca. NCI-H460	0.8	Brain (Hippocampus) Pool	1.5
Lung ca. HOP-62	10.2	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	4.9	Brain (Substantia nigra) Pool	0.2
Liver	0.0	Brain (Thalamus) Pool	1.2
Fetal Liver	1.2	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.4
Kidney Pool	3.1	Adrenal Gland	2.0
Fetal Kidney	0.0	Pituitary gland Pool	1.8
Renal ca. 786-0	6.3	Salivary Gland	3.2
Renal ca. A498	0.0	Thyroid (female)	3.8
Renal ca. ACHN	12.1	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	3.2	Pancreas Pool	4.2

Table AKC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3542, Run 166453844	Tissue Name	Rel. Exp.(%) Ag3542, Run 166453844
Secondary Th1 act	3.9	HUVEC IL-1beta	0.0
Secondary Th2 act	5.4	HUVEC IFN gamma	2.4
Secondary Tr1 act	3.8	HUVEC TNF alpha + IFN gamma	0.4
Secondary Th1 rest	33.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	5.3	HUVEC IL-11	1.4
Secondary Tr1 rest	14.8	Lung Microvascular EC none	3.1
Primary Th1 act	6.1	Lung Microvascular EC TNFalpha + IL-1beta	1.9
Primary Th2 act	0.6	Microvascular Dermal EC none	1.9
Primary Tr1 act	5.5	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	84.7	Bronchial epithelium TNFalpha + IL-1beta	2.7
Primary Tr1 rest	16.0	Small airway epithelium TNFalpha + IL-1beta	3.8

CD45RA CD4 lymphocyte act	0.3	Coronary artery SMC rest	2.1
CD45RO CD4 lymphocyte act	3.6	Coronary artery SMC TNFalpha + IL-1beta	0.5
CD8 lymphocyte act	0.9	Astrocytes rest	5.8
Secondary CD8 lymphocyte rest	2.5	Astrocytes TNFalpha + IL-1beta	12.0
Secondary CD8 lymphocyte act	12.6	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	13.6	KU-812 (Basophil) PMA/ionomycin	5.4
2ry Th1/Th2/Tr1_anti-CD95 CH11	40.6	CCD1106 (Keratinocytes) none	1.7
LAK cells rest	3.7	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	4.9
LAK cells IL-2	7.6	Liver cirrhosis	81.2
LAK cells IL-2+IL-12	7.9	Lupus kidney	5.0
LAK cells IL-2+IFN gamma	11.7	NCI-H292 none	7.8
LAK cells IL-2+ IL-18	7.2	NCI-H292 IL-4	3.5
LAK cells PMA/ionomycin	3.8	NCI-H292 IL-9	6.0
NK Cells IL-2 rest	8.0	NCI-H292 IL-13	6.4
Two Way MLR 3 day	2.3	NCI-H292 IFN gamma	2.4
Two Way MLR 5 day	0.9	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.9
PBMC rest	12.8	Lung fibroblast none	0.0
PBMC PWM	5.4	Lung fibroblast TNF alpha + IL-1 beta	1.1
PBMC PHA-L	3.7	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	1.9
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.4
B lymphocytes PWM	3.7	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	4.4	Dermal fibroblast CCD1070 rest	0.4
EOL-1 dbcAMP	14.1	Dermal fibroblast CCD1070 TNF alpha	18.0
Dendritic cells none		Dermal fibroblast IFN gamma	
Dendritic cells LPS	1.4	Dermal fibroblast IL-4	1.4

Dendritic cells anti-CD40	2.3	IBD Colitis 2	4.0
Monocytes rest	53.2	IBD Crohn's	3.2
Monocytes LPS	19.2	Colon	100.0
Macrophages rest	0.6	Lung	11.1
Macrophages LPS	0.0	Thymus	2.7
HUVEC none	5.4	Kidney	7.7
HUVEC starved	4.3		

CNS_neurodegeneration_v1.0 Summary: Ag3542 Expression of the CG59315-01 gene is low/undetectable in all the samples on this panel. (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3542 Expression of the CG59315-01 gene is highest in a breast cancer cell line (CT=31.3). Furthermore, there is significant expression in a cluster of cell lines derived from brain cancer, colon cancer and ovarian cancer. Therefore, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of colon, brain, ovarian, and breast cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon, brain, ovarian, and breast cancers.

Low but significant levels of expression are also seen in the cerebellum. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

Among metabolic tissues, this gene is expressed at low levels in adipose. Therefore, this gene product may be useful in the treatment of obesity.

Panel 4D Summary: Ag3542 Expression of the CG59315-01 gene is highest in the normal colon (CT=30). Furthermore, expression is undetectable in colon samples from Crohn's and colitis patients. Thus, expression of this gene could be used to differentiate between normal and inflamed colon. This gene encodes a connexin homolog, a gap junction protein involved in intercellular communication.

therapeutic antibodies that block its function may also be used in the treatment of a number of inflammatory and autoimmune diseases in which T cells and monocytes play a pivotal role.

These include, but are not limited to, Crohn's disease, ulcerative colitis, multiple sclerosis, chronic obstructive pulmonary disease, asthma, emphysema, rheumatoid arthritis, lupus erythematosus, or psoriasis.

References:

1. Kwak BR, Mulhaupt F, Veillard N, Gros DB, Mach F. Altered pattern of vascular connexin expression in atherosclerotic plaques. *Arterioscler Thromb Vasc Biol* 2002 Feb 1;22(2):225-30

AL. CG59203-01: Lysozyme C-like protein

Expression of gene CG59203-01 was assessed using the primer-probe set Ag3392, described in Table ALA. Results of the RTQ-PCR runs are shown in Tables ALB and ALC.

Table ALA. Probe Name Ag3392

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tgtgaggtttcctaaactggaa-3'	22	540	511
Probe	TET-5'-ctttgcagcaacgccttagggttt-3'- TAMRA	24	576	512
Reverse	5'-tgacacaggcatttggacat-3'	20	607	513

Table ALB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3392, Run 216821373	Tissue Name	Rel. Exp.(%) Ag3392, Run 216821373
Adipose	0.0	Renal ca. TK-10	2.7
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.7
Melanoma* M14	1.2	Gastric ca. KATO III	0.4
Melanoma* I OXIMVI	0.0	Colon ca. SW-948	0.6
Squamous cell carcinoma SCC-4	0.0	Colon ca. (SW48 met) SW620	0.0

Testis Pool	100.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	1.2
Placenta	0.7	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.4	Colon ca. Colo-205	11.6
Ovarian ca. SK-OV-3	1.0	Colon ca. SW-48	2.2
Ovarian ca. OVCAR-4	0.0	Colon Pool	1.1
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.4
Ovarian ca. IGROV-1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	1.3
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	15.2	Heart Pool	1.1
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	1.7	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.5
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.9
Trachea	1.1	CNS cancer (glio/astro) U87-MG	1.4
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.5
Fetal Lung	0.8	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	5.4	CNS cancer (astro) SNB-75	6.1
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. NCI-H25	0.0	Brain (Cerebrum)	0.0
Lung ca. NCI-H460	1.1	Brain (Hippocampus)	0.0

		Pool	
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.5
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	0.0
Liver	1.5	Brain (Thalamus) Pool	0.9
Fetal Liver	1.2	Brain (whole)	0.0
Liver ca. HepG2	18.3	Spinal Cord Pool	0.0
Kidney Pool	1.6	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	0.0
Renal ca. 786-0	0.3	Salivary Gland	0.0
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

Table ALC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3392, Run 165296470	Tissue Name	Rel. Exp.(%) Ag3392, Run 165296470
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	36.9	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4			
lymphocyte act		TNFalpha + IL-1beta	
CD8 lymphocyte act	0.0	Astrocytes rest	0.0

Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	100.0
LAK cells IL-2+IL-12	0.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	0.0
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	16.8	NCI-H292 IL-9	0.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	11.1	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	26.8	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Monocytes LPS	0.0	Colon	0.0

Macrophages rest	0.0	Lung	0.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3392 Expression of the CG59203-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3392 Highest expression of the CG59203-01 gene is seen in the testis. Thus, expression of this gene could be used as a marker of testicular tissue. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in treating infertility or hypogonadism.

Panel 4D Summary: Ag3392 Significant expression of this gene is detected in a liver cirrhosis sample (CT = 33.8). Furthermore, expression of this gene is not detected in normal liver in Panel 1.3D, suggesting that its expression is unique to liver cirrhosis. Therefore, therapeutic modulation of the expression or function of this gene may reduce or inhibit fibrosis that occurs in liver cirrhosis. In addition, expression of this gene could also be used for the diagnosis of liver cirrhosis.

AM. CG58662-01: cytoplasmic protein

Expression of gene CG58662-01 was assessed using the primer-probe set Ag3387, described in Table AMA. Results of the RTQ-PCR runs are shown in Tables AMB, AMC and AMD.

Table AMA. Probe Name Ag3387

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-aacctgcactcctccatga-3'	19	504	514
Probe	TET-5'-agaccccagcagggtatcctctgag-3'-TAMRA	25	532	515
Reverse	5'-ctctgtcagtgcccacatct-3'	20	564	516

Table AMB. CNS_neurodegeneration_v1.0

Sample	Ag3392	Ag3387
AD 1 Hippo	15.7	7.3
Control (Path) 2		
Temporal Ctx		

AD 2 Hippo	34.6	Control (Path) 4 Temporal Ctx	42.0
AD 3 Hippo	5.5	AD 1 Occipital Ctx	17.9
AD 4 Hippo	9.7	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	95.3	AD 3 Occipital Ctx	5.4
AD 6 Hippo	33.9	AD 4 Occipital Ctx	19.6
Control 2 Hippo	41.5	AD 5 Occipital Ctx	61.1
Control 4 Hippo	9.0	AD 6 Occipital Ctx	19.5
Control (Path) 3 Hippo	6.7	Control 1 Occipital Ctx	5.8
AD 1 Temporal Ctx	11.2	Control 2 Occipital Ctx	83.5
AD 2 Temporal Ctx	37.6	Control 3 Occipital Ctx	19.3
AD 3 Temporal Ctx	4.0	Control 4 Occipital Ctx	5.0
AD 4 Temporal Ctx	21.5	Control (Path) 1 Occipital Ctx	88.9
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	13.4
AD 5 Sup Temporal Ctx	37.9	Control (Path) 3 Occipital Ctx	5.8
AD 6 Inf Temporal Ctx	35.6	Control (Path) 4 Occipital Ctx	24.3
AD 6 Sup Temporal Ctx	39.2	Control 1 Parietal Ctx	9.4
Control 1 Temporal Ctx	6.7	Control 2 Parietal Ctx	44.4
Control 2 Temporal Ctx	65.5	Control 3 Parietal Ctx	28.5
Control 3 Temporal Ctx	19.3	Control (Path) 1 Parietal Ctx	90.8
Control 3 Temporal Ctx	11.4	Control (Path) 2 Parietal Ctx	25.7
Control (Path) 1 Temporal Ctx	83.5	Control (Path) 3 Parietal Ctx	5.6
Control (Path) 2 Temporal Ctx	56.6	Control (Path) 4 Parietal Ctx	56.6

Table AMC. General screening panel v1.4

Tissue Name		Tissue Name	
Run 217043912		Run 217043912	
Adipose	8.2	Renal ca. TK-10	66.4

Melanoma* Hs688(A).T	30.6	Bladder	11.2
Melanoma* Hs688(B).T	34.6	Gastric ca. (liver met.) NCI-N87	15.3
Melanoma* M14	27.0	Gastric ca. KATO III	20.6
Melanoma* LOXIMVI	17.6	Colon ca. SW-948	1.1
Melanoma* SK- MEL-5	25.3	Colon ca. SW480	33.0
Squamous cell carcinoma SCC-4	5.7	Colon ca.* (SW480 met) SW620	29.9
Testis Pool	17.8	Colon ca. HT29	8.8
Prostate ca.* (bone met) PC-3	27.7	Colon ca. HCT-116	15.4
Prostate Pool	16.0	Colon ca. CaCo-2	13.1
Placenta	11.0	Colon cancer tissue	13.8
Uterus Pool	1.7	Colon ca. SW1116	7.9
Ovarian ca. OVCAR-3	17.0	Colon ca. Colo-205	4.4
Ovarian ca. SK-OV- 3	11.3	Colon ca. SW-48	9.3
Ovarian ca. OVCAR-4	7.1	Colon Pool	20.4
Ovarian ca. OVCAR-5	37.4	Small Intestine Pool	12.5
Ovarian ca. IGROV- 1	23.7	Stomach Pool	12.1
Ovarian ca. OVCAR-8	16.8	Bone Marrow Pool	4.3
Ovary	20.0	Fetal Heart	18.7
Breast ca. MCF-7	5.6	Heart Pool	12.3
Breast ca. MDA- MB-231	41.5	Lymph Node Pool	18.9
Breast ca. BT 549	55.1	Fetal Skeletal Muscle	8.9
Breast ca. T47D	63.3	Skeletal Muscle Pool	23.2
Breast ca. MDA-N	23.5	Spleen Pool	10.8
Breast Pool	25.5	Thymus Pool	18.0
Trachea	13.6	CNS cancer (glio/astro) U87-MG	62.4
Lung	5.3	CNS cancer (glio/astro) U87-MG	12.5
Lung ca. NCI-N417	6.2	CNS cancer (astro) SF- 539	17.3

Lung ca. LX-1	33.7	CNS cancer (astro) SNB-75	27.2
Lung ca. NCI-H146	10.0	CNS cancer (glio) SNB-19	25.9
Lung ca. SHP-77	39.2	CNS cancer (glio) SF- 295	54.0
Lung ca. A549	43.8	Brain (Amygdala) Pool	47.6
Lung ca. NCI-H526	6.5	Brain (cerebellum)	90.1
Lung ca. NCI-H23	44.8	Brain (fetal)	56.6
Lung ca. NCI-H460	23.8	Brain (Hippocampus) Pool	45.7
Lung ca. HOP-62	53.6	Cerebral Cortex Pool	60.3
Lung ca. NCI-H522	100.0	Brain (Substantia nigra) Pool	61.6
Liver	4.4	Brain (Thalamus) Pool	75.8
Fetal Liver	17.0	Brain (whole)	63.3
Liver ca. HepG2	33.9	Spinal Cord Pool	24.1
Kidney Pool	37.1	Adrenal Gland	23.5
Fetal Kidney	16.4	Pituitary gland Pool	3.9
Renal ca. 786-0	14.8	Salivary Gland	9.9
Renal ca. A498	7.5	Thyroid (female)	29.1
Renal ca. ACHN	26.2	Pancreatic ca. CAPAN2	39.8
Renal ca. UO-31	81.8	Pancreas Pool	49.3

Table AMD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3387, Run 165296475	Tissue Name	Rel. Exp.(%) Ag3387, Run 165296475
Secondary Th1 act	24.1	HUVEC IL-1beta	12.1
Secondary Th2 act	29.9	HUVEC IFN gamma	27.0
Secondary Tr1 act	26.2	HUVEC TNF alpha + IFN gamma	19.1
Secondary Th1 rest	18.9	HUVEC TNF alpha + IL4	16.0
Secondary Th2 rest	22.8	HUVEC IL-11	16.4
Secondary Tr1 rest	28.1	Lung Microvascular EC none	36.6
Primary Th1 act	12.4	Lung Microvascular EC TNFalpha + IL-1beta	27.2
		Microvascular Dermal EC	
		Microvascular Dermal EC TNFalpha + IL-1beta	
Primary Th1 rest	46.0	Bronchial epithelium	18.0

		TNFalpha + IL1beta	
Primary Th2 rest	36.1	Small airway epithelium none	3.9
Primary Tr1 rest	37.6	Small airway epithelium TNFalpha + IL-1beta	33.2
CD45RA CD4 lymphocyte act	5.7	Coronary artery SMC rest	19.6
CD45RO CD4 lymphocyte act	19.9	Coronary artery SMC TNFalpha + IL-1beta	12.7
CD8 lymphocyte act	16.2	Astrocytes rest	27.9
Secondary CD8 lymphocyte rest	11.3	Astrocytes TNFalpha + IL-1beta	21.8
Secondary CD8 lymphocyte act	12.3	KU-812 (Basophil) rest	7.6
CD4 lymphocyte none	5.7	KU-812 (Basophil) PMA/ionomycin	22.1
2ry Th1/Th2/Tr1_anti-CD95 CH11	12.2	CCD1106 (Keratinocytes) none	12.0
LAK cells rest	19.2	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	19.3
LAK cells IL-2	25.9	Liver cirrhosis	9.4
LAK cells IL-2+IL-12	10.2	Lupus kidney	3.2
LAK cells IL-2+IFN gamma	26.4	NCI-H292 none	62.0
LAK cells IL-2+ IL-18	21.2	NCI-H292 IL-4	71.2
LAK cells PMA/ionomycin	4.2	NCI-H292 IL-9	52.5
NK Cells IL-2 rest	21.2	NCI-H292 IL-13	24.8
Two Way MLR 3 day	30.6	NCI-H292 IFN gamma	33.7
Two Way MLR 5 day	26.2	HPAEC none	27.7
Two Way MLR 7 day	16.8	HPAEC TNF alpha + IL-1 beta	12.6
PBMC rest	10.7	Lung fibroblast none	25.3
PBMC PWM	21.3	Lung fibroblast TNF alpha + IL-1 beta	12.1
PBMC PHA-L	25.5	Lung fibroblast IL-4	48.0
Ramos (B cell) none	18.4	Lung fibroblast IL-9	34.6
Ramos (B cell) ionomycin	68.3	Lung fibroblast IL-13	51.1
B lymphocytes PWM	54.0	Lung fibroblast IFN gamma	63.3
EOL-1 dbcAMP	18.4	Dermal fibroblast CCD1070 TNF alpha	74.2

EOL-1 dbcAMP PMA/ionomycin	3.1	Dermal fibroblast CCD1070 IL-1 beta	4.6
Dendritic cells none	28.1	Dermal fibroblast IFN gamma	10.1
Dendritic cells LPS	29.7	Dermal fibroblast IL-4	23.8
Dendritic cells anti- CD40	19.6	IBD Colitis 2	1.4
Monocytes rest	17.2	IBD Crohn's	2.4
Monocytes LPS	1.6	Colon	21.8
Macrophages rest	30.8	Lung	16.6
Macrophages LPS	17.4	Thymus	100.0
HUVEC none	22.8	Kidney	48.0
HUVEC starved	28.5		

CNS_neurodegeneration_v1.0 Summary: Ag3387 This panel does not show differential expression of the CG58662-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.3D for discussion of utility of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3387 Expression of the CG58662-01 gene is ubiquitous in this panel, with highest expression in a lung cancer cell line (CT=29.5). In addition, this gene is expressed at higher levels in kidney cancer cell lines when compared to normal kidney expression. Thus, expression of this gene could be used to differentiate these samples from other samples and as a marker for these cancers. Furthermore, therapeutic modulation of the expression of function of this gene may be effective in the treatment of lung and kidney cancer.

Among metabolic tissues this gene is expressed at moderate to low levels in adipose, adrenal gland, pancreas, pituitary, and adult and fetal skeletal muscle, heart and liver. This widespread expression among these tissues suggests that this gene plays a role in normal metabolic and neuroendocrine function and that dysregulated expression of this gene may contribute to neuroendocrine diseases or metabolic disorders, such as obesity and diabetes.

In addition, this gene is expressed at moderate to low levels in all CNS regions examined and may be a small molecule target for the treatment of neurologic diseases, such

Panel 4D Summary: Ag3387 The CG58662-01 gene is expressed at high to moderate levels in a wide range of cell types of significance in the immune response in health and disease, with highest expression in the thymus (CT=31). In addition, expression is seen in members of the T-cell, B-cell, endothelial cell, macrophage/monocyte, and peripheral blood mononuclear cell family, as well as epithelial and fibroblast cell types from lung and skin, and normal tissues represented by colon, lung, thymus and kidney. This ubiquitous pattern of expression suggests that this gene product may be involved in homeostatic processes for these and other cell types and tissues. This pattern is in agreement with the expression profile in General_screening_panel_v1.5 and also suggests a role for the gene product in cell survival and proliferation. Therefore, modulation of the gene product with a functional therapeutic may lead to the alteration of functions associated with these cell types and lead to improvement of the symptoms of patients suffering from autoimmune and inflammatory diseases such as asthma, allergies, inflammatory bowel disease, lupus erythematosus, psoriasis, rheumatoid arthritis, and osteoarthritis.

AN. CG59371-01: Novel cytoplasmic protein

Expression of gene CG59371-01 was assessed using the primer-probe set Ag3558, described in Table ANA. Results of the RTQ-PCR runs are shown in Tables ANB, ANC, AND and ANE.

Table ANA. Probe Name Ag3558

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cttgaggctgagaaggagaag-3'	21	208	517
Probe	TET-5'-tgcttatcaactcacagagaaggaca-3'-TAMRA	26	231	518
Reverse	5'-gttggtctctcagtcgctgta-3'	21	263	519

Table ANB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3558, Run 213391281	Tissue Name	Rel. Exp.(%) Ag3558, Run 213391281
Adipose	0.4	Renal ca TK-10	14.3
Melanoma* Hs688(B).T	2.2	Gastric ca JTC-9	0.4
		NCI-N87	0.4

Melanoma* M14	41.5	Gastric ca. KATO III	82.9
Melanoma* LOXIMVI	30.1	Colon ca. SW-948	14.8
Melanoma* SK-MEL-5	23.8	Colon ca. SW480	81.2
Squamous cell carcinoma SCC-4	34.6	Colon ca.* (SW480 met) SW620	24.0
Testis Pool	7.6	Colon ca. HT29	20.6
Prostate ca.* (bone met) PC-3	9.7	Colon ca. HCT-116	61.6
Prostate Pool	0.1	Colon ca. CaCo-2	17.7
Placenta	0.3	Colon cancer tissue	7.7
Uterus Pool	0.1	Colon ca. SW1116	6.9
Ovarian ca. OVCAR-3	15.3	Colon ca. Colo-205	3.2
Ovarian ca. SK-OV-3	62.0	Colon ca. SW-48	9.3
Ovarian ca. OVCAR-4	27.5	Colon Pool	0.3
Ovarian ca. OVCAR-5	14.4	Small Intestine Pool	0.1
Ovarian ca. IGROV-1	5.8	Stomach Pool	2.0
Ovarian ca. OVCAR-8	2.5	Bone Marrow Pool	0.3
Ovary	0.2	Fetal Heart	3.3
Breast ca. MCF-7	15.5	Heart Pool	0.0
Breast ca. MDA-MB-231	100.0	Lymph Node Pool	0.5
Breast ca. BT 549	72.7	Fetal Skeletal Muscle	0.7
Breast ca. T47D	17.1	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	13.5	Spleen Pool	0.8
Breast Pool	0.2	Thymus Pool	7.2
Trachea	0.4	CNS cancer (glio/astro) U87-MG	17.6
Lung	0.0	CNS cancer (glio/astro) U-118-MG	61.6
Fetal Lung	2.5	CNS cancer (neuro;met) SK-N-AS	14.9
Lung ca. NCI-N417	5.4	CNS cancer (astro) SF-531	21.6
Lung ca. NCI-H146	15.2	CNS cancer (glio) SNB-19	4.6

Lung ca. SHP-77	42.0	CNS cancer (glio) SF-295	0.8
Lung ca. A549	28.5	Brain (Amygdala) Pool	0.1
Lung ca. NCI-H526	6.4	Brain (cerebellum)	0.0
Lung ca. NCI-H23	21.3	Brain (fetal)	1.1
Lung ca. NCI-H460	0.7	Brain (Hippocampus) Pool	0.2
Lung ca. HOP-62	4.7	Cerebral Cortex Pool	0.1
Lung ca. NCI-H522	23.8	Brain (Substantia nigra) Pool	0.1
Liver	0.0	Brain (Thalamus) Pool	0.0
Fetal Liver	0.8	Brain (whole)	0.0
Liver ca. HepG2	7.7	Spinal Cord Pool	0.1
Kidney Pool	0.1	Adrenal Gland	0.2
Fetal Kidney	4.1	Pituitary gland Pool	0.0
Renal ca. 786-0	52.5	Salivary Gland	0.0
Renal ca. A498	6.5	Thyroid (female)	0.2
Renal ca. ACHN	14.0	Pancreatic ca. CAPAN2	43.2
Renal ca. UO-31	20.2	Pancreas Pool	0.9

Table ANC. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag3558, Run 248592792	Tissue Name	Rel. Exp.(%) Ag3558, Run 248592792
Adipose	0.4	Renal ca. TK-10	16.6
Melanoma* Hs688(A).T	2.0	Bladder	3.3
Melanoma* Hs688(B).T	3.1	Gastric ca. (liver met.) NCI-N87	6.7
Melanoma* M14	34.9	Gastric ca. KATO III	93.3
Melanoma* LOXIMVI	26.4	Colon ca. SW-948	13.0
Melanoma* SK-MEL-5	29.5	Colon ca. SW480	76.3
Squamous cell carcinoma SCC-4	33.0	Colon ca.* (SW480 met) SW620	25.5
Testis Pool	7.2	Colon ca. HT29	18.8
Prostate ca.* (bone met) PC-3	10.3	Colon ca. HCT-116	55.5
Prostate ca. PC-9	1.1	Colon ca. CaCo-2	23.5
Fetus Pool	0.0	Colon ca. SW620	0.0
Ovarian ca.	29.5	Colon ca. Colo-205	5.0

OVCAR-3			
Ovarian ca. SK-OV-3	40.6	Colon ca. SW-48	6.8
Ovarian ca. OVCAR-4	29.5	Colon Pool	0.2
Ovarian ca. OVCAR-5	11.7	Small Intestine Pool	0.2
Ovarian ca. IGROV-1	4.6	Stomach Pool	0.2
Ovarian ca. OVCAR-8	5.2	Bone Marrow Pool	0.2
Ovary	0.2	Fetal Heart	2.0
Breast ca. MCF-7	18.0	Heart Pool	0.0
Breast ca. MDA-MB-231	85.3	Lymph Node Pool	0.5
Breast ca. BT 549	100.0	Fetal Skeletal Muscle	0.8
Breast ca. T47D	23.3	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	20.2	Spleen Pool	1.0
Breast Pool	0.3	Thymus Pool	3.7
Trachea	0.4	CNS cancer (glio/astro) U87-MG	15.4
Lung	0.0	CNS cancer (glio/astro) U-118-MG	64.6
Fetal Lung	3.5	CNS cancer (neuro;met) SK-N-AS	24.7
Lung ca. NCI-N417	5.0	CNS cancer (astro) SF-539	21.6
Lung ca. LX-1	32.1	CNS cancer (astro) SNB-75	30.4
Lung ca. NCI-H146	13.6	CNS cancer (glio) SNB-19	4.8
Lung ca. SHP-77	34.9	CNS cancer (glio) SF-295	3.3
Lung ca. A549	35.4	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	3.4	Brain (cerebellum)	0.0
Lung ca. NCI-H23	15.9	Brain (fetal)	0.7
Lung ca. NCI-H460	0.4	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	4.5	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	25.5	Brain (Substantia nigra) Pool	0.0
Brain (whole)			
Liver ca. HepG2	6.6	Spinal Cord Pool	0.0

Kidney Pool	0.1	Adrenal Gland	0.1
Fetal Kidney	4.6	Pituitary gland Pool	0.0
Renal ca. 786-0	44.1	Salivary Gland	0.0
Renal ca. A498	4.2	Thyroid (female)	0.1
Renal ca. ACHN	15.2	Pancreatic ca. CAPAN2	48.3
Renal ca. UO-31	20.4	Pancreas Pool	0.5

Table AND. Panel 2.2

Tissue Name	Rel. Exp.(%) Ag3558, Run 173762113	Rel. Exp.(%) Ag3558, Run 174924057	Tissue Name	Rel. Exp.(%) Ag3558, Run 173762113	Rel. Exp.(%) Ag3558, Run 174924057
Normal Colon	12.5	5.6	Kidney Margin (OD04348)	3.3	1.1
Colon cancer (OD06064)	100.0	100.0	Kidney malignant cancer (OD06204B)	5.6	8.9
Colon Margin (OD06064)	27.5	17.7	Kidney normal adjacent tissue (OD06204E)	0.6	0.3
Colon cancer (OD06159)	3.1	4.8	Kidney Cancer (OD04450-01)	6.3	2.8
Colon Margin (OD06159)	5.6	7.3	Kidney Margin (OD04450-03)	0.6	0.0
Colon cancer (OD06297-04)	11.5	16.6	Kidney Cancer 8120613	0.0	0.0
Colon Margin (OD06297-05)	12.5	7.8	Kidney Margin 8120614	0.3	0.3
CC Gr.2 ascend colon (ODO3921)	6.9	5.7	Kidney Cancer 9010320	0.2	1.9
CC Margin (ODO3921)	6.8	6.4	Kidney Margin 9010321	2.1	2.3
Colon cancer metastasis (OD06104)	6.8	4.9	Kidney Cancer 8120607	0.8	1.7
Lung Margin (OD06104)	17.9	12.6	Kidney Margin 8120608	0.3	0.0
Colon mets to lung (OD04451-)	15.1	23.3	Normal Uterus	1.6	0.5
Normal Prostate	2.1	0.0	Normal Thyroid	0.3	0.0

Prostate Cancer (OD04410)	0.0	0.2	Thyroid Cancer 064010	1.1	0.7
Prostate Margin (OD04410)	0.4	0.3	Thyroid Cancer A302152	1.2	1.0
Normal Ovary	2.7	0.4	Thyroid Margin A302153	0.3	0.3
Ovarian cancer (OD06283-03)	30.1	32.8	Normal Breast	2.7	1.9
Ovarian Margin (OD06283-07)	1.4	1.3	Breast Cancer (OD04566)	7.4	8.5
Ovarian Cancer 064008	7.0	1.9	Breast Cancer 1024	4.3	6.5
Ovarian cancer (OD06145)	1.2	1.9	Breast Cancer (OD04590-01)	11.8	13.9
Ovarian Margin (OD06145)	0.9	0.6	Breast Cancer Mets (OD04590-03)	8.0	6.8
Ovarian cancer (OD06455-03)	28.1	30.4	Breast Cancer Metastasis (OD04655-05)	7.9	11.0
Ovarian Margin (OD06455-07)	0.7	0.6	Breast Cancer 064006	5.7	5.8
Normal Lung	1.4	1.3	Breast Cancer 9100266	0.7	0.3
Invasive poor diff. lung adeno (ODO4945-01)	25.0	20.3	Breast Margin 9100265	1.8	1.1
Lung Margin (ODO4945-03)	1.0	1.7	Breast Cancer A209073	2.5	1.2
Lung Malignant Cancer (OD03126)	6.3	6.4	Breast Margin A2090734	3.0	1.2
Lung Margin (OD03126)	1.3	1.0	Breast cancer (OD06083)	15.7	24.7
Lung Cancer (OD05014A)	13.5	10.3	Breast cancer node metastasis (OD06083)	16.5	15.0
Lung Margin (OD05014B)	3.1	4.8	Normal Liver	0.0	0.0
Lung cancer (OD06081)	38.4	28.7	Liver Cancer 1026	1.2	0.0
Lung Margin			Liver Cancer		
Lung Margin	0.8	1.9	Liver Tissue	2.2	1.4

(OD04237-02)			6004-N		
Ocular Melanoma Metastasis	0.2	0.6	Liver Cancer 6005-T	0.8	1.0
Ocular Melanoma Margin (Liver)	0.0	0.0	Liver Tissue 6005-N	1.3	0.3
Melanoma Metastasis	13.2	12.5	Liver Cancer 064003	1.6	2.0
Melanoma Margin (Lung)	1.6	1.1	Normal Bladder	4.4	4.4
Normal Kidney	0.3	0.0	Bladder Cancer 1023	4.6	1.9
Kidney Ca, Nuclear grade 2 (OD04338)	0.0	1.0	Bladder Cancer A302173	23.0	15.4
Kidney Margin (OD04338)	0.8	0.3	Normal Stomach	6.5	9.5
Kidney Ca Nuclear grade 1/2 (OD04339)	0.6	2.6	Gastric Cancer 9060397	2.9	3.2
Kidney Margin (OD04339)	0.8	0.6	Stomach Margin 9060396	4.9	1.0
Kidney Ca, Clear cell type (OD04340)	0.6	1.2	Gastric Cancer 9060395	6.3	4.6
Kidney Margin (OD04340)	0.7	1.4	Stomach Margin 9060394	3.5	3.0
Kidney Ca, Nuclear grade 3 (OD04348)	36.9	31.0	Gastric Cancer 064005	22.1	20.0

Table ANE. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3558, Run 166488678	Tissue Name	Rel. Exp.(%) Ag3558, Run 166488678
Secondary Th1 act	17.9	HUVEC IL-1beta	10.3
Secondary Th2 act	12.4	HUVEC IFN gamma	12.2
		HUVEC TNF alpha + IFN	
Secondary Th2 rest	2.1	HUVEC IL-1	2.1
Secondary Tr1 rest	2.5	Lung Microvascular EC	5.2

		none	
Primary Th1 act	9.1	Lung Microvascular EC TNFalpha + IL-1beta	4.8
Primary Th2 act	11.6	Microvascular Dermal EC none	19.5
Primary Tr1 act	11.4	Microvascular Dermal EC TNFalpha + IL-1beta	8.5
Primary Th1 rest	32.8	Bronchial epithelium TNFalpha + IL1beta	1.0
Primary Th2 rest	10.4	Small airway epithelium none	0.5
Primary Tr1 rest	13.4	Small airway epithelium TNFalpha + IL-1beta	5.8
CD45RA CD4 lymphocyte act	10.7	Coronary artery SMC rest	2.3
CD45RO CD4 lymphocyte act	17.2	Coronary artery SMC TNFalpha + IL-1beta	1.3
CD8 lymphocyte act	12.2	Astrocytes rest	1.4
Secondary CD8 lymphocyte rest	11.7	Astrocytes TNFalpha + IL-1beta	0.7
Secondary CD8 lymphocyte act	10.4	KU-812 (Basophil) rest	3.1
CD4 lymphocyte none	0.1	KU-812 (Basophil) PMA/ionomycin	6.6
2ry Th1/Th2/Tr1_anti- CD95 CH11	6.0	CCD1106 (Keratinocytes) none	11.3
LAK cells rest	1.8	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	2.6
LAK cells IL-2	16.3	Liver cirrhosis	0.3
LAK cells IL-2+IL-12	9.7	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	19.9	NCI-H292 none	12.2
LAK cells IL-2+ IL-18	16.4	NCI-H292 IL-4	29.7
LAK cells PMA/ionomycin	0.7	NCI-H292 IL-9	24.3
NK Cells IL-2 rest	9.9	NCI-H292 IL-13	16.4
Two Way MLR 3 day	1.5	NCI-H292 IFN gamma	16.0
Two Way MLR 5 day	7.4	HPAEC none	8.9
Two Way MLR 7 day	6.1	HPAEC TNF alpha + IL-1 beta	5.5
PMBC PHA-L	23.5	Lung fibroblast IL-4	0.5
Ramos (B cell) none	13.4	Lung fibroblast IL-9	2.3

Ramos (B cell) ionomycin	47.0	Lung fibroblast IL-13	0.5
B lymphocytes PWM	79.0	Lung fibroblast IFN gamma	0.5
B lymphocytes CD40L and IL-4	16.2	Dermal fibroblast CCD1070 rest	48.6
EOL-1 dbcAMP	6.3	Dermal fibroblast CCD1070 TNF alpha	100.0
EOL-1 dbcAMP PMA/ionomycin	4.5	Dermal fibroblast CCD1070 IL-1 beta	25.5
Dendritic cells none	1.1	Dermal fibroblast IFN gamma	14.0
Dendritic cells LPS	0.1	Dermal fibroblast IL-4	14.9
Dendritic cells anti- CD40	0.1	IBD Colitis 2	0.5
Monocytes rest	0.0	IBD Crohn's	0.2
Monocytes LPS	0.0	Colon	1.7
Macrophages rest	3.0	Lung	1.2
Macrophages LPS	0.4	Thymus	0.0
HUVEC none	18.7	Kidney	11.4
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3558 Expression of the CG59371-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3558 Highest expression of the CG59371-01 gene is seen in a breast cancer cell line (CT=23.4). Overall, expression of this gene is significantly higher in cancer cell lines and fetal derived tissues than in samples derived from normal adult tissues. There are significant levels of expression in clusters of cell lines derived from pancreatic, brain, colon, gastric, renal, lung, ovarian, breast and melanoma cancers. Thus, expression of this gene in could be used to differentiate between the cancer derived samples and fetal tissues from other samples on this panel and as a marker to detect the presence of cancer. Furthermore, the much higher levels of expression in proliferative tissue suggest that this gene may be involved in cell proliferation. Therefore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of these cancers.

Among tissues with metabolic function, this gene is expressed at moderate to low

levels. The widespread expression among these tissues suggests that the gene product may play a role in normal neuroendocrine and metabolic and that dysregulated

expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

This molecule is a novel protein phosphatase expressed at moderate to low levels in all regions of the CNS examined. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

General_screening_panel_v1.5 Summary: Ag3558 Results from this experiment are in excellent agreement with results from Panel 1.4. Please see that panel for discussion of utility of this gene in cancer, metabolic disorders and the central nervous system.

Panel 2.2 Summary: Ag3558 Two experiments with the same probe and primer produce results that are in excellent agreement, with highest expression of the CG59371-01 gene in colon cancer (CTs=30). Furthermore, expression is higher in kidney, lung, ovary and colon cancers when compared to normal adjacent tissue. In addition, significant expression is also seen in gastric, breast, and bladder cancer. Thus, , expression of this gene in could be used to differentiate between the cancer derived samples and other samples on this panel and as a marker to detect the presence of cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of these cancers.

Panel 4D Summary: Ag3558 The CG59371-01 gene is widely expressed among the samples on this panel, with highest expression in dermal fibroblasts treated with TNF-alpha. Significant levels of expression are also seen in treated and untreated samples from skin, lung, T-cells and B-cells. Therefore, modulation of the expression or activity of the protein encoded by this transcript through the application of antibodies or peptides therapeutics may be beneficial for the treatment of lung inflammatory diseases such as asthma, and chronic obstructive pulmonary diseases, inflammatory skin diseases such as psoriasis, atopic dermatitis, ulcerative dermatitis, and ulcerative colitis, autoimmune diseases such as Crohn's disease, lupus erythematosus, rheumatoid arthritis and osteoarthritis and in other diseases in which T cells and B cells are activated.

CG59371-01 (P1) (P2) (P3) (P4) (P5) (P6) (P7) (P8) (P9) (P10)

Expression of gene CG59346-01 was assessed using the primer-probe set Ag3550, described in Table AOA. Results of the RTQ-PCR runs are shown in Tables AOB, AOC and AOD.

Table AOA. Probe Name Ag3550

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gccaacagagatgaacaaagag-3'	22	3459	520
Probe	TET-5'-accgcctctccttctcccgtct-3'-TAMRA	23	3508	521
Reverse	5'-ttggaaggctaaagacatctga-3'	22	3532	522

Table AOB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3550, Run 210641081	Tissue Name	Rel. Exp.(%) Ag3550, Run 210641081
AD 1 Hippo	12.8	Control (Path) 3 Temporal Ctx	5.1
AD 2 Hippo	38.7	Control (Path) 4 Temporal Ctx	40.3
AD 3 Hippo	10.4	AD 1 Occipital Ctx	18.8
AD 4 Hippo	15.8	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	79.6	AD 3 Occipital Ctx	7.2
AD 6 Hippo	49.3	AD 4 Occipital Ctx	25.9
Control 2 Hippo	37.4	AD 5 Occipital Ctx	37.6
Control 4 Hippo	10.3	AD 6 Occipital Ctx	19.6
Control (Path) 3 Hippo	9.6	Control 1 Occipital Ctx	2.1
AD 1 Temporal Ctx	15.7	Control 2 Occipital Ctx	56.6
AD 2 Temporal Ctx	37.1	Control 3 Occipital Ctx	26.8
AD 3 Temporal Ctx	8.6	Control 4 Occipital Ctx	5.0
AD 4 Temporal Ctx	30.6	Control (Path) 1 Occipital Ctx	93.3
AD 5 Inf Temporal Ctx	66.9	Control (Path) 2 Occipital Ctx	14.6
AD 6 Inf Temporal Ctx	65.4	Control (Path) 3 Occipital Ctx	10.1

AD 6 Sup Temporal Ctx	53.2	Control 1 Parietal Ctx	8.7
Control 1 Temporal Ctx	7.3	Control 2 Parietal Ctx	48.0
Control 2 Temporal Ctx	36.6	Control 3 Parietal Ctx	17.2
Control 3 Temporal Ctx	29.7	Control (Path) 1 Parietal Ctx	84.1
Control 3 Temporal Ctx	14.6	Control (Path) 2 Parietal Ctx	28.5
Control (Path) 1 Temporal Ctx	100.0	Control (Path) 3 Parietal Ctx	4.6
Control (Path) 2 Temporal Ctx	65.5	Control (Path) 4 Parietal Ctx	56.6

Table AOC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3550, Run 217048931	Tissue Name	Rel. Exp.(%) Ag3550, Run 217048931
Adipose	0.5	Renal ca. TK-10	27.7
Melanoma* Hs688(A).T	1.4	Bladder	13.7
Melanoma* Hs688(B).T	1.6	Gastric ca. (liver met.) NCI-N87	25.0
Melanoma* M14	0.0	Gastric ca. KATO III	24.5
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	1.4
Melanoma* SK-MEL-5	0.8	Colon ca. SW480	8.8
Squamous cell carcinoma SCC-4	2.1	Colon ca.* (SW480 met) SW620	7.4
Testis Pool	2.0	Colon ca. HT29	2.0
Prostate ca.* (bone met) PC-3	15.2	Colon ca. HCT-116	7.1
Prostate Pool	6.7	Colon ca. CaCo-2	92.0
Placenta	18.9	Colon cancer tissue	6.0
Uterus Pool	0.0	Colon ca. SW1116	1.8
Ovarian ca. OVCAR-3	7.6	Colon ca. Colo-205	3.0
Ovarian ca. SK-OV-3	14.9	Colon ca. SW-48	3.1
Ovarian ca. OVCAR-5	24.5	Small Intestine Pool	5.0

Ovarian ca. IGROV-1	2.1	Stomach Pool	6.9
Ovarian ca. OVCAR-8	2.4	Bone Marrow Pool	0.2
Ovary	1.4	Fetal Heart	0.1
Breast ca. MCF-7	34.6	Heart Pool	0.1
Breast ca. MDA-MB-231	8.2	Lymph Node Pool	2.8
Breast ca. BT 549	0.2	Fetal Skeletal Muscle	0.2
Breast ca. T47D	57.4	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	1.8
Breast Pool	4.6	Thymus Pool	7.2
Trachea	14.1	CNS cancer (glio/astro) U87-MG	0.1
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.1
Fetal Lung	19.5	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	1.5	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	24.7	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	7.4	CNS cancer (glio) SNB-19	2.1
Lung ca. SHP-77	0.2	CNS cancer (glio) SF-295	0.1
Lung ca. A549	26.1	Brain (Amygdala) Pool	22.1
Lung ca. NCI-H526	13.9	Brain (cerebellum)	63.3
Lung ca. NCI-H23	6.6	Brain (fetal)	100.0
Lung ca. NCI-H460	11.1	Brain (Hippocampus) Pool	28.1
Lung ca. HOP-62	0.2	Cerebral Cortex Pool	34.2
Lung ca. NCI-H522	0.5	Brain (Substantia nigra) Pool	26.2
Liver	3.6	Brain (Thalamus) Pool	37.9
Fetal Liver	19.1	Brain (whole)	57.8
Liver ca. HepG2	26.4	Spinal Cord Pool	2.8
Kidney Pool	0.3	Adrenal Gland	2.6
Fetal Kidney	11.7	Pituitary gland Pool	3.6
Renal ca. 786-0	23.3	Salivary Gland	25.5
Renal ca. UO 31	12.7	Pancreas Pool	12.7

Table AOD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3550, Run 166453850	Tissue Name	Rel. Exp.(%) Ag3550, Run 166453850
Secondary Th1 act	0.2	HUVEC IL-1beta	0.0
Secondary Th2 act	0.1	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	9.5
Primary Th2 rest	0.0	Small airway epithelium none	8.1
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	27.2
CD45RA CD4 lymphocyte act	1.4	Coronary artery SMC rest	0.7
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	1.0
CD8 lymphocyte act	0.0	Astrocytes rest	5.2
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	5.9
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.1
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	10.5
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	23.0
LAK cells IL-2	0.0	Liver cirrhosis	22.8
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	81.8

LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	69.7
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	58.6
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	61.1
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	57.4
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	45.7
PBMC PHA-L	0.0	Lung fibroblast IL-4	36.6
Ramos (B cell) none	0.0	Lung fibroblast IL-9	33.9
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	17.2
B lymphocytes PWM	2.4	Lung fibroblast IFN gamma	34.9
B lymphocytes CD40L and IL-4	11.3	Dermal fibroblast CCD1070 rest	28.5
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	11.3
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	4.8
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.3
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti- CD40	0.3	IBD Colitis 2	6.9
Monocytes rest	36.3	IBD Crohn's	2.0
Monocytes LPS	0.0	Colon	36.6
Macrophages rest	0.0	Lung	14.3
Macrophages LPS	0.0	Thymus	100.0
HUVEC none	0.0	Kidney	0.1
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3550 This panel does not show differential expression of the CG59346-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.4 for discussion of utility of this gene in the central nervous system.

cerebral cortex, and thalamus and at moderate levels in the amygdala, hippocampus, and

thalamus. This CG59346-01 gene encodes a homologue of Proline-rich synapse-associated protein-1/cortactin binding protein 1 (ProSAP1/CortBP1). ProSAP1 is PDZ-domain protein highly enriched in the postsynaptic density (PSD) and involved in the assembly of the PSD during neuronal differentiation that may function with contactin, in the recruitment and activation of neural intracellular signaling pathways. Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

In addition, moderate levels of expression are seen in colon, gastric, renal, pancreatic, lung, ovarian, breast and prostate cancer cell lines. Thus, expression of this gene could be used to detect the presence of cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of these cancers.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in pituitary, adipose, adrenal gland, pancreas, thyroid, and adult and fetal and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

In addition, this gene is expressed at higher levels in fetal lung and kidney (CTs=29) when compared to expression in adult lung and kidney (CTs=35-40). Thus, expression of this gene could be used to differentiate between the two sources of lung and kidney tissue.

References:

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2. Boeckers TM, Kreutz MR, Winter C, Zuschratter W, Smalla KH, Sanmarti-Vila L, Wex H, Langnaese K, Bockmann J, Garner CC, Gundelfinger ED. (1999) Proline-rich synapse-associated protein-1/cortactin binding protein 1 (ProSAP1/CortBP1) is a PDZ-domain

Panel 4D Summary: Ag3550 Highest expression of the CG59346-01 gene is seen in thymus (CT=27). In addition, significant levels of expression are seen in IL-4, IL-9, IL-13 and IFN gamma activated-NCI-H292 mucoepidermoid cells as well as untreated NCI-H292 cells. Moderate/low expression is also detected in IL-4, IL-9, IL-13 and IFN gamma activated lung fibroblasts, small airway epithelium (treated and untreated), and treated bronchial epithelium. The expression of this gene in cells derived from or within the lung suggests that this gene may be involved in normal conditions as well as pathological and inflammatory lung disorders that include chronic obstructive pulmonary disease, asthma, allergy and emphysema.

In addition, significant levels of expression are seen in treated and untreated dermal fibroblasts and keratinocytes, suggesting that modulation of the expression or function of this gene may also reduce symptoms in inflammatory skin diseases such as psoriasis, atopic dermatitis, and ulcerative dermatitis.

AP. CG57814-01 and CG57814-02: Basic I 19 protein

Expression of gene CG57814-01 and varian CG57814-02 was assessed using the primer-probe set Ag791, described in Table APA.

Table APA. Probe Name Ag791

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-aaatgtgatgaccaagggttctg-3'	22	1290	523
Probe	TET-5'-agcacacattatccagcgaaagcatg-3'-TAMRA	26	1319	524
Reverse	5'-tgtcaaagaaacccttggtgtc-3'	22	1368	525

Panel 1.2 Summary: Ag791 Expression of the CG57814-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

AQ. CG59327-01: MONOCARBOXYLATE TRANSPORTER 1 like protein

Expression of gene CG59327-01 was assessed using the primer-probe set Ag3548, described in Table AQA. Results of the RTQ-PCR runs are shown in Tables AQB and AQC.

Primers	Sequences	Length	Start Position	SEQ ID NO:
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Forward	5'-atttgcatacagcagctttgtc-3'	22	517	526
Probe	TET-5'-ttcatctcccagaaatcgtaatttg-3'- TAMRA	26	549	527
Reverse	5'-accttcgcttgctccaataagt-3'	22	579	528

Table AQB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3548, Run 217048438	Tissue Name	Rel. Exp.(%) Ag3548, Run 217048438
Adipose	0.0	Renal ca. TK-10	3.6
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	1.3
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	0.0
Testis Pool	0.0	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	0.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.0
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	1.2	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	2.2
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0
Ovarian ca. IGROV- 1	0.0	Stomach Pool	0.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. BT 249	0.0	Fetal Skeletal Muscle	0.0

Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.0
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	0.0
Lung	2.4	CNS cancer (glio/astro) U-118-MG	6.5
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF- 539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	6.4
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHIP-77	0.0	CNS cancer (glio) SF- 295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	0.0
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.0	Brain (fetal)	0.0
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	0.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	0.0
Lung ca. NCI-H522	3.1	Brain (Substantia nigra) Pool	0.0
Liver	0.0	Brain (Thalamus) Pool	0.0
Fetal Liver	0.0	Brain (whole)	0.0
Liver ca. HepG2	0.0	Spinal Cord Pool	0.0
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	3.4	Pituitary gland Pool	0.0
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. A498	100.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.0
Renal ca. UO-31	0.0	Pancreas Pool	0.0

Table AQC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3548, Run 166453848	Tissue Name	Rel. Exp.(%) Ag3548, Run 166453848
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	0.0

Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.5
Secondary Tr1 rest	0.0	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	100.0
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.2
Primary Th2 rest	0.0	Small airway epithelium none	1.2
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.3
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.3
2ry Th1/Th2/Tr1_anti- CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	6.5
LAK cells IL-2+IL-12	0.0	Lupus kidney	0.7
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	1.8
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	1.7
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	0.2
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.0
Two Way MLR 5 day	0.0	HPAEC none	0.5
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha	0.0

		+ IL-1 beta	
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.0
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	0.0
Dendritic cells anti-CD40	0.0	IBD Colitis 2	2.0
Monocytes rest	0.0	IBD Crohn's	3.5
Monocytes LPS	0.0	Colon	1.0
Macrophages rest	0.0	Lung	2.3
Macrophages LPS	0.0	Thymus	0.7
HUVEC none	0.0	Kidney	0.0
HUVEC starved	0.4		

CNS_neurodegeneration_v1.0 Summary: Ag3548 Expression of the CG59327-01 gene is low/undetectable in all the samples on the panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3548 Significant expression of the CG59327-01 gene is restricted to a sample derived from a kidney cancer cell line (CT=33.34). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker to detect the presence of kidney cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of kidney cancer.

Panel 4D Summary: Ag3548 Significant expression of the CG59327-01 gene is restricted to a samples derived from untreated microvascular dermal endothelial cells (CT=30.3). Thus,

AK. CG59494-01: Myelin P2

Expression of gene CG59494-01, which represents a full length physical clone, was assessed using the primer-probe set Ag3206, described in Table ARA. Results of the RTQ-PCR runs are shown in Tables ARB and ARC.

Table ARA. Probe Name Ag3206

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-agtgttgatgggaaaatgatga-3'	22	160	455
Probe	TET-5'-ccataagaacagaaagttctttccaggaca-3'-TAMRA	30	182	758
Reverse	5'-ccccagcttgaaggagatc-3'	19	216	759

Table ARB. Panel 1.3D

Tissue Name	Rel. Exp.(%) Ag3206, Run 165527079	Tissue Name	Rel. Exp.(%) Ag3206, Run 165527079
Liver adenocarcinoma	0.0	Kidney (fetal)	10.5
Pancreas	0.0	Renal ca. 786-0	0.0
Pancreatic ca. CAPAN 2	17.8	Renal ca. A498	15.6
Adrenal gland	0.0	Renal ca. RXF 393	0.0
Thyroid	0.0	Renal ca. ACHN	14.8
Salivary gland	0.0	Renal ca. UO-31	0.0
Pituitary gland	0.0	Renal ca. TK-10	0.0
Brain (fetal)	0.0	Liver	0.0
Brain (whole)	9.9	Liver (fetal)	0.0
Brain (amygdala)	0.0	Liver ca. (hepatoblast) HepG2	0.0
Brain (cerebellum)	0.0	Lung	0.0
Brain (hippocampus)	0.0	Lung (fetal)	0.0
Brain (substantia nigra)	0.0	Lung ca. (small cell) LX-1	4.5
Brain (thalamus)	0.0	Lung ca. (small cell) NCI-H69	0.0
Cerebral Cortex	0.0	Lung ca. (s.cell var.) SHP-77	18.0
Spinal cord	33.4	Lung ca. (large cell) NCI-H460	41.2
glio astro (H23-MC)	0.0	Lung ca. (large cell) NCI-H23	0.0

astrocytoma SW1783	0.0	Lung ca. (non-s.cell) HOP-62	0.0
neuro*; met SK-N-AS	0.0	Lung ca. (non-s.cl) NCI-H522	0.0
astrocytoma SF-539	0.0	Lung ca. (squam.) SW 900	0.0
astrocytoma SNB-75	11.7	Lung ca. (squam.) NCI-H596	0.0
glioma SNB-19	0.0	Mammary gland	14.4
glioma U251	0.0	Breast ca.* (pl.ef) MCF-7	0.0
glioma SF-295	0.0	Breast ca.* (pl.ef) MDA-MB-231	0.0
Heart (fetal)	0.0	Breast ca.* (pl.ef) T47D	0.0
Heart	15.5	Breast ca. BT-549	0.0
Skeletal muscle (fetal)	0.0	Breast ca. MDA-N	0.0
Skeletal muscle	0.0	Ovary	0.0
Bone marrow	0.0	Ovarian ca. OVCAR-3	14.0
Thymus	0.0	Ovarian ca. OVCAR-4	0.0
Spleen	0.0	Ovarian ca. OVCAR-5	0.0
Lymph node	0.0	Ovarian ca. OVCAR-8	0.0
Colorectal	0.0	Ovarian ca. IGROV-1	11.6
Stomach	0.0	Ovarian ca.* (ascites) SK-OV-3	0.0
Small intestine	0.0	Uterus	0.0
Colon ca. SW480	0.0	Placenta	0.0
Colon ca.* SW620(SW480 met)	0.0	Prostate	0.0
Colon ca. HT29	0.0	Prostate ca.* (bone met)PC-3	100.0
Colon ca. HCT-116	0.0	Testis	27.5
Colon ca. CaCo-2	42.0	Melanoma Hs688(A).T	0.0
Colon ca. tissue(ODO3866)	0.0	Melanoma* (met) Hs688(B).T	0.0
NCI NSC Melanoma cell			
Bladder	0.0	Melanoma LOX	0.0

		IMVI	
Trachea	0.0	Melanoma* (mct) SK-MEL-5	0.0
Kidney	0.0	Adipose	0.0

Table ARC. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3206, Run 164531735	Tissue Name	Rel. Exp.(%) Ag3206, Run 164531735
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	11.9	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.0	HUVEC TNF alpha + IFN gamma	12.6
Secondary Th1 rest	11.9	HUVEC TNF alpha + IL4	15.9
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	75.8
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	100.0
Primary Th2 act	0.0	Microvascular Dermal EC none	72.2
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.0	Small airway epithelium none	0.0
Primary Tr1 rest	0.0	Small airway epithelium TNFalpha + IL-1beta	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0
CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	0.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA ionomycin	0.0
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0

LAK cells IL-2	0.0	Liver cirrhosis	29.7
LAK cells IL-2+IL-12	0.0	Lupus kidney	0.0
LAK cells IL-2+IFN gamma	0.0	NCI-H292 none	97.3
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	43.8
NK Cells IL-2 rest	7.8	NCI-H292 IL-13	24.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	12.7
Two Way MLR 5 day	0.0	HPAEC none	14.3
Two Way MLR 7 day	0.0	HPAEC TNF alpha + IL-1 beta	33.2
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.0
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	16.2
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	15.9
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.0
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.0
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells none	0.0	Dermal fibroblast IFN gamma	0.0
Dendritic cells LPS	0.0	Dermal fibroblast IL-4	15.0
Dendritic cells anti-CD40	0.0	IBD Colitis 2	27.4
Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	0.0	Colon	6.7
Macrophages rest	0.0	Lung	0.0
Macrophages LPS	0.0	Thymus	0.0
HUVEC none	27.7	Kidney	0.0
HUVEC starved	20.0		

Panel 1.3D Summary: Ag3206 Expression of the CG59494-01 gene is restricted to a sample

used to differentiate between (a) sample and other samples, (b) this panel, and (c) other panels.

detect the presence of prostate cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of prostate cancer.

Panel 4D Summary: Ag3206 Expression of the CG59494-01 gene is primarily restricted to a cluster of samples derived from microvasculature of the lung and the dermis suggesting a role for this gene in the maintenance of the integrity of the microvasculature. Therefore, therapeutics designed for this putative protein could be beneficial for the treatment of diseases associated with damaged microvasculature including heart diseases or inflammatory diseases, such as psoriasis, asthma, and chronic obstructive pulmonary diseases.

AS. CG59432-01 and CG59432-02: Chloride Channel

Expression of gene CG59432-01 and CG59432-02 was assessed using the primer-probe set Ag5938, described in Table ASA. Results of the RTQ-PCR runs are shown in Tables ASB and ASC. Please note that CG59432-02 represents a full-length physical clone of CG59432-01 gene, validating the prediction of the gene sequence.

Table ASA. Probe Name Ag5938

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-ttgtgtcagtcctataccattaa-3'	22	626	529
Probe	TET-5'-accagcttgccctctgtccagt-3'-TAMRA	22	658	530
Reverse	5'-tcctggagttcagagtatatct-3'	22	710	531

Table ASB. General_screening_panel_v1.5

Tissue Name	Rel. Exp.(%) Ag5938, Run 248102142	Tissue Name	Rel. Exp.(%) Ag5938, Run 248102142
Adipose	6.3	Renal ca. TK-10	2.7
Melanoma* Hs688(A).T	0.0	Bladder	17.6
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	100.0
Melanoma* M14	0.0	Gastric ca. KATO III	8.2
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Squamous cell carcinoma SCC-4	21.5	Colon ca * (SW 480 met) SW620	0.6

Testis Pool	21.0	Colon ca. HT29	7.1
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	11.0
Prostate Pool	6.9	Colon ca. CaCo-2	25.2
Placenta	0.0	Colon cancer tissue	4.7
Uterus Pool	1.5	Colon ca. SW1116	2.7
Ovarian ca. OVCAR-3	20.2	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	5.7
Ovarian ca. OVCAR-5	24.7	Small Intestine Pool	7.6
Ovarian ca. IGROV-1	0.0	Stomach Pool	3.2
Ovarian ca. OVCAR-8	2.8	Bone Marrow Pool	6.6
Ovary	0.0	Fetal Heart	1.0
Breast ca. MCF-7	4.2	Heart Pool	4.3
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	3.8
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	59.9
Breast ca. T47D	0.0	Skeletal Muscle Pool	93.3
Breast ca. MDA-N	0.0	Spleen Pool	3.2
Breast Pool	10.4	Thymus Pool	3.6
Trachea	15.1	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.6	CNS cancer (glio/astro) U-118-MG	3.1
Fetal Lung	31.6	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	3.2	CNS cancer (glio) SNB-19	3.6
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	17.2
Lung ca. NCI-H127	0.0	Brain (Hippocampus)	15.8
Lung ca. NCI-H460	0.0	Brain (Hippocampus)	15.8

		Pool	
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	27.0
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	25.2
Liver	0.0	Brain (Thalamus) Pool	29.1
Fetal Liver	7.0	Brain (whole)	9.5
Liver ca. HepG2	0.0	Spinal Cord Pool	11.0
Kidney Pool	6.8	Adrenal Gland	8.4
Fetal Kidney	17.1	Pituitary gland Pool	6.3
Renal ca. 786-0	0.0	Salivary Gland	4.8
Renal ca. A498	0.0	Thyroid (female)	0.0
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	1.4
Renal ca. UO-31	0.0	Pancreas Pool	4.5

Table ASC. Panel 5 Islet

Tissue Name	Rel. Exp.(%) Ag5938, Run 248045753	Tissue Name	Rel. Exp.(%) Ag5938, Run 248045753
97457_Patient-02go_adipose	0.0	94709_Donor 2 AM - A_adipose	0.0
97476_Patient-07sk_skeletal muscle	0.0	94710_Donor 2 AM - B_adipose	0.0
97477_Patient-07ut_uterus	0.0	94711_Donor 2 AM - C_adipose	0.0
97478_Patient-07pl_placenta	1.1	94712_Donor 2 AD - A_adipose	0.0
99167_Bayer Patient 1	0.0	94713_Donor 2 AD - B_adipose	0.0
97482_Patient-08ut_uterus	0.0	94714_Donor 2 AD - C_adipose	0.0
97483_Patient-08pl_placenta	0.0	94742_Donor 3 U - A_Mesenchymal Stem Cells	0.0
97486_Patient-09sk_skeletal muscle	0.0	94743_Donor 3 U - B_Mesenchymal Stem Cells	0.0
97487_Patient-09ut_uterus	0.0	94730_Donor 3 AM - A_adipose	0.7
97488_Patient-09pl_placenta	0.5	94731_Donor 3 AM - B_adipose	0.0
97492_Patient-10ut_uterus	0.0	94732_Donor 3 AM - C_adipose	0.0
97498_Patient-11go_adipose		94734_Donor 3 AD - B_adipose	

97496_Patient-11sk_skeletal muscle	2.4	94735_Donor 3 AD - C_adipose	0.0
97497_Patient-11ut_uterus	0.0	77138_Liver_HepG2untreated	0.0
97498_Patient-11pl_placenta	0.0	73556_Heart_Cardiac stromal cells (primary)	0.0
97500_Patient-12go_adipose	0.7	81735_Small Intestine	100.0
97501_Patient-12sk_skeletal muscle	6.8	72409_Kidney_Proximal Convoluted Tubule	0.0
97502_Patient-12ut_uterus	0.0	82685_Small intestine_Duodenum	4.6
97503_Patient-12pl_placenta	0.0	90650_Adrenal_Adrenocortical adenoma	0.0
94721_Donor 2 U - A_Mesenchymal Stem Cells	0.0	72410_Kidney_HRCE	0.0
94722_Donor 2 U - B_Mesenchymal Stem Cells	0.0	72411_Kidney_HRE	0.0
94723_Donor 2 U - C_Mesenchymal Stem Cells	6.5	73139_Uterus_Uterine smooth muscle cells	0.0

General_screening_panel_v1.5 Summary: Ag5938 Highest expression of the CG59432-01 gene is seen in a gastric cancer cell line (CT=32.5). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel. In addition, low expression of this gene is seen in colon cancer CaCo-2, lung cancer NCI-H526, ovarian cancer OVCAR-5, and squamous cell carcinoma SCC-4 cell lines. Therefore, therapeutic modulation of the activity of this gene or its protein product, through the use of small molecule drugs, protein therapeutics or antibodies, might be beneficial in the treatment of these cancers.

Significant expression is also detected in fetal skeletal muscle and adult skeletal muscle (CT=32.5). At least 50 disease-causing mutations in the skeletal muscle voltage-gated chloride channel gene (CLCN1), almost all of which originate from Caucasian families, have been identified. Therefore, therapeutic modulation of this gene product, a chloride channel homolog, may be a treatment for myotonia congenita and other muscle channelopathies.

Therefore, this gene may play a role in central nervous system disorders such as Alzheimer's disease, Parkinson's disease, epilepsy, multiple sclerosis, schizophrenia and depression.

References:

1. Sasaki R, Ito N, Shimamura M, Murakami T, Kuzuhara S, Uchino M, Uyama E. A novel CLCN1 mutation: P480T in a Japanese family with Thomsen's myotonia congenita. Muscle Nerve. 2001 Mar;24(3):357-63.

Panel 5 Islet Summary: Ag5938 Expression of the CG59432-01 is restricted to a sample from small intestine (CT=31.6). Thus, expression of this gene could be used to differentiate between this sample and other samples on this panel and as a marker for this tissue.

AT. CG59383-01: D6MM5E

Expression of gene CG59383-01 was assessed using the primer-probe set Ag3427, described in Table ATA. Results of the RTQ-PCR runs are shown in Tables ATB, ATC and ATD.

Table ATA. Probe Name Ag3427

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5' -cagtgaacagaccaagaaca-3'	21	784	532
Probe	TET-5' -tctttcttcacagtgttcagcaaca-3' - TAMRA	26	817	533
Reverse	5' -ggattatctctgggtctggaa-3'	21	844	534

Table ATB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3427, Run 210351187	Tissue Name	Rel. Exp.(%) Ag3427, Run 210351187
AD 1 Hippo	11.4	Control (Path) 3 Temporal Ctx	2.0
AD 2 Hippo	50.3	Control (Path) 4 Temporal Ctx	23.3
AD 3 Hippo	10.2	AD 1 Occipital Ctx	9.8
AD 5 Hippo	4.2	AD 3 Occipital Ctx	1.0
AD 6 Hippo	42.9	AD 4 Occipital Ctx	17.0

Control 2 Hippo	21.2	AD 5 Occipital Ctx	25.3
Control 4 Hippo	6.1	AD 6 Occipital Ctx	29.9
Control (Path) 3 Hippo	15.1	Control 1 Occipital Ctx	3.0
AD 1 Temporal Ctx	22.7	Control 2 Occipital Ctx	32.3
AD 2 Temporal Ctx	45.1	Control 3 Occipital Ctx	26.2
AD 3 Temporal Ctx	6.0	Control 4 Occipital Ctx	8.4
AD 4 Temporal Ctx	39.0	Control (Path) 1 Occipital Ctx	84.1
AD 5 Inf Temporal Ctx	100.0	Control (Path) 2 Occipital Ctx	11.7
AD 5 Sup Temporal Ctx	53.6	Control (Path) 3 Occipital Ctx	0.9
AD 6 Inf Temporal Ctx	57.0	Control (Path) 4 Occipital Ctx	10.3
AD 6 Sup Temporal Ctx	58.2	Control 1 Parietal Ctx	6.4
Control 1 Temporal Ctx	18.8	Control 2 Parietal Ctx	48.6
Control 2 Temporal Ctx	51.1	Control 3 Parietal Ctx	38.7
Control 3 Temporal Ctx	16.5	Control (Path) 1 Parietal Ctx	54.7
Control 3 Temporal Ctx	5.5	Control (Path) 2 Parietal Ctx	8.4
Control (Path) 1 Temporal Ctx	82.9	Control (Path) 3 Parietal Ctx	1.4
Control (Path) 2 Temporal Ctx	33.0	Control (Path) 4 Parietal Ctx	16.2

Table ATC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3427, Run 216821480	Tissue Name	Rel. Exp.(%) Ag3427, Run 216821480
Adipose	0.5	Renal ca. TK-10	8.4
Melanoma* Hs688(A).T	0.0	Bladder	1.7
Melanoma*		Gastric ca. (liver met.)	
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0

Melanoma* SK-MEL-5	0.2	Colon ca. SW480	0.4
Squamous cell carcinoma SCC-4	14.5	Colon ca.* (SW480 met) SW620	0.1
Testis Pool	10.7	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	100.0
Prostate Pool	0.0	Colon ca. CaCo-2	0.1
Placenta	0.2	Colon cancer tissue	1.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	2.9	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV-3	50.7	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	2.1	Colon Pool	0.4
Ovarian ca. OVCAR-5	1.1	Small Intestine Pool	0.3
Ovarian ca. IGROV-1	9.7	Stomach Pool	0.9
Ovarian ca. OVCAR-8	13.7	Bone Marrow Pool	0.4
Ovary	0.2	Fetal Heart	0.0
Breast ca. MCF-7	0.1	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.4
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.2
Breast ca. T47D	2.1	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	0.2
Breast Pool	1.7	Thymus Pool	1.4
Trachea	1.7	CNS cancer (glio/astro) U87-MG	0.0
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.4
Fetal Lung	0.4	CNS cancer (neuro;met) SK-N-AS	0.1
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.3	CNS cancer (astro) SNB-75	0.8
NSC 66059			
295			
Lung ca. A549	0.0	Brain (Amygdala) Pool	1.7

Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.9
Lung ca. NCI-H23	0.2	Brain (fetal)	0.1
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	2.2
Lung ca. HOP-62	0.5	Cerebral Cortex Pool	1.7
Lung ca. NCI-H522	0.1	Brain (Substantia nigra) Pool	1.0
Liver	0.0	Brain (Thalamus) Pool	2.9
Fetal Liver	0.1	Brain (whole)	1.7
Liver ca. HepG2	0.0	Spinal Cord Pool	0.2
Kidney Pool	0.2	Adrenal Gland	0.4
Fetal Kidney	0.8	Pituitary gland Pool	1.3
Renal ca. 786-0	0.1	Salivary Gland	0.6
Renal ca. A498	0.1	Thyroid (female)	1.9
Renal ca. ACHN	0.0	Pancreatic ca. CAPAN2	0.1
Renal ca. UO-31	0.5	Pancreas Pool	2.3

Table ATD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3427, Run 166396769	Tissue Name	Rel. Exp.(%) Ag3427, Run 166396769
Secondary Th1 act	1.4	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.8	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	1.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	2.9	Lung Microvascular EC none	0.0
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	0.0
Primary Tr1 act	4.9	Microvascular Dermal EC TNFalpha + IL-1beta	0.0
Primary Th1 rest	2.5	Bronchial epithelium TNFalpha + IL1beta	7.9
Primary Th2 rest	2.0	Small airway epithelium none	0.0
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0

CD45RO CD4 lymphocyte act	0.9	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	5.0
Secondary CD8 lymphocyte rest	1.0	Astrocytes TNFalpha + IL-1beta	2.4
Secondary CD8 lymphocyte act	0.8	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	2.0	CCD1106 (Keratinocytes) none	28.5
LAK cells rest	0.0	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	100.0
LAK cells IL-2	0.0	Liver cirrhosis	23.8
LAK cells IL-2+IL-12	1.6	Lupus kidney	3.4
LAK cells IL-2+IFN gamma	3.7	NCI H292 none	1.8
LAK cells IL-2+ IL-18	0.9	NCI-H292 IL-4	3.8
LAK cells PMA/ionomycin	0.0	NCI-H292 IL-9	2.0
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	4.0
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	1.1
Two Way MLR 5 day	0.0	HPAEC none	0.0
Two Way MLR 7 day	0.9	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	0.7	Lung fibroblast TNF alpha + IL-1 beta	0.8
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.7
Ramos (B cell) ionomycin	0.0	Lung fibroblast IL-13	0.0
B lymphocytes PWM	3.4	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	4.0	Dermal fibroblast CCD1070 rest	0.9
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	5.6
EOL-1 dbcAMP PMA/ionomycin	1.1	Dermal fibroblast CCD1070 IL-1 beta	0.0
Dendritic cells anti-CD40	0.0	IBD Colitis 2	5.9

Monocytes rest	0.0	IBD Crohn's	2.4
Monocytes LPS	0.0	Colon	4.1
Macrophages rest	0.0	Lung	1.7
Macrophages LPS	0.0	Thymus	12.4
HUVEC none	0.0	Kidney	10.2
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3427 This panel confirms the expression of CG59383-01 gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. Please see Panel 1.4 for a discussion of the potential utility of this gene in treatment of central nervous system disorders.

General_screening_panel_v1.4 Summary: Ag3427 Highest expression of the CG59383-01 gene is seen in a colon cancer cell line (CT=27.2). Significant expression is also seen in a cluster of samples derived from ovarian cancer cell lines. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker for the presence of these cancers. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of ovarian or colon cancers.

This molecule is also expressed at low levels in all regions of the CNS examined. Therefore, therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

Among tissues with metabolic function, this gene is expressed at low levels in adipose and pancreas. This expression suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes

Panel 4D Summary: Ag3427 Highest expression of the CG59383-01 gene is seen in keratinocytes treated with the inflammatory cytokines TNF-alpha and IL-1 beta (CT=30.3).

asthma, COPD, emphysema, psoriasis and wound healing

AU. CG58526-01: Scramblase

Expression of gene CG58526-01 was assessed using the primer-probe set Ag3366, described in Table AUA. Results of the RTQ-PCR runs are shown in Table AUB.

Table AUA. Probe Name Ag3366

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-tgtcttcacaaatgctgacaat-3'	22	729	535
Probe	TET-5'-ttcggaattcatgttcctgcagatct-3'- TAMRA	26	751	536
Reverse	5'-gatcattgctgctttgactgtt-3'	22	783	537

Table AUB. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3366, Run 217042585	Tissue Name	Rel. Exp.(%) Ag3366, Run 217042585
Adipose	0.0	Renal ca. TK-10	0.0
Melanoma* Hs688(A).T	0.0	Bladder	0.0
Melanoma* Hs688(B).T	0.0	Gastric ca. (liver met.) NCI-N87	0.0
Melanoma* M14	0.0	Gastric ca. KATO III	0.0
Melanoma* LOXIMVI	0.0	Colon ca. SW-948	0.0
Melanoma* SK- MEL-5	0.0	Colon ca. SW480	0.0
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	100.0
Testis Pool	69.3	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.0	Colon ca. HCT-116	25.2
Prostate Pool	0.0	Colon ca. CaCo-2	43.2
Placenta	0.0	Colon cancer tissue	0.0
Uterus Pool	0.0	Colon ca. SW1116	0.0
Ovarian ca. OVCAR-3	0.0	Colon ca. Colo-205	0.0
Ovarian ca. SK-OV- 3	0.0	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-5	0.0	Small Intestine Pool	0.0

Ovarian ca. IGROV-1	0.0	Stomach Pool	49.0
Ovarian ca. OVCAR-8	0.0	Bone Marrow Pool	0.0
Ovary	0.0	Fetal Heart	0.0
Breast ca. MCF-7	0.0	Heart Pool	0.0
Breast ca. MDA-MB-231	0.0	Lymph Node Pool	0.0
Breast ca. BT 549	0.0	Fetal Skeletal Muscle	0.0
Breast ca. T47D	0.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	0.0	Spleen Pool	3.9
Breast Pool	0.0	Thymus Pool	0.0
Trachea	0.0	CNS cancer (glio/astro) U87-MG	3.5
Lung	0.0	CNS cancer (glio/astro) U-118-MG	0.0
Fetal Lung	0.0	CNS cancer (neuro;met) SK-N-AS	0.0
Lung ca. NCI-N417	0.0	CNS cancer (astro) SF-539	0.0
Lung ca. LX-1	0.0	CNS cancer (astro) SNB-75	0.0
Lung ca. NCI-H146	0.0	CNS cancer (glio) SNB-19	0.0
Lung ca. SHP-77	0.0	CNS cancer (glio) SF-295	0.0
Lung ca. A549	0.0	Brain (Amygdala) Pool	12.5
Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.0
Lung ca. NCI-H23	0.0	Brain (fetal)	13.8
Lung ca. NCI-H460	0.0	Brain (Hippocampus) Pool	15.0
Lung ca. HOP-62	0.0	Cerebral Cortex Pool	2.6
Lung ca. NCI-H522	0.0	Brain (Substantia nigra) Pool	7.5
Liver	0.0	Brain (Thalamus) Pool	15.7
Fetal Liver	0.0	Brain (whole)	15.2
Liver ca. HepG2	0.0	Spinal Cord Pool	7.5
Kidney Pool	0.0	Adrenal Gland	0.0
Fetal Kidney	0.0	Pituitary gland Pool	22.8
Renal ca. 786-0	0.0	Salivary Gland	0.0
Renal ca. UO-51		Pancreas Pool	

CNS_neurodegeneration_v1.0 Summary: Ag3366 Expression of the CG58526-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3366 Expression of the CG58526-01 gene is restricted to a sample derived from a colon cancer cell line (CT=34.5) and the testis. Thus, expression of this gene could be used to differentiate between these samples and other samples on this panel and as a marker to detect the presence of colon cancer. Furthermore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of colon cancer.

Panel 4D Summary: Ag3366 Results from one experiment with the CG58526-01 gene are not included. The amp plot indicates that there were experimental difficulties with this run.

AV. CG57851-01: sulfotransferase

Expression of gene CG57851-01 was assessed using the primer-probe set Ag3349, described in Table AVA. Results of the RTQ-PCR runs are shown in Tables AVB, AVC and AVD.

Table AVA. Probe Name Ag3349

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-acaaaatgatggcgatattgag-3'	22	237	538
Probe	TET-5'-cgcttcattcaactcaacacct-3'-TAMRA	25	270	539
Reverse	5'-tcattcttattccactccaggaa-3'	22	295	540

Table AVB. CNS_neurodegeneration_v1.0

Tissue Name	Rel. Exp.(%) Ag3349, Run 210141483	Tissue Name	Rel. Exp.(%) Ag3349, Run 210141483
AD 1 Hippo	32.8	Control (Path) 3 Temporal Ctx	0.0
AD 2 Hippo	61.6	Control (Path) 4 Temporal Ctx	48.6
AD 3 Hippo	18.0	AD 1 Occipital Ctx	10.5
AD 5 Hippo	11.7	AD 3 Occipital Ctx	0.0
AD 6 Hippo	11.7	AD 4 Occipital Ctx	0.0

Control 2 Hippo	27.4	AD 5 Occipital Ctx	8.6
Control 4 Hippo	17.9	AD 6 Occipital Ctx	0.0
Control (Path) 3 Hippo	12.7	Control 1 Occipital Ctx	0.0
AD 1 Temporal Ctx	14.8	Control 2 Occipital Ctx	0.0
AD 2 Temporal Ctx	8.7	Control 3 Occipital Ctx	51.4
AD 3 Temporal Ctx	8.2	Control 4 Occipital Ctx	5.6
AD 4 Temporal Ctx	10.4	Control (Path) 1 Occipital Ctx	100.0
AD 5 Inf Temporal Ctx	7.2	Control (Path) 2 Occipital Ctx	17.8
AD 5 Sup Temporal Ctx	7.4	Control (Path) 3 Occipital Ctx	0.0
AD 6 Inf Temporal Ctx	9.1	Control (Path) 4 Occipital Ctx	41.2
AD 6 Sup Temporal Ctx	27.9	Control 1 Parietal Ctx	3.3
Control 1 Temporal Ctx	9.2	Control 2 Parietal Ctx	70.7
Control 2 Temporal Ctx	25.9	Control 3 Parietal Ctx	14.3
Control 3 Temporal Ctx	13.4	Control (Path) 1 Parietal Ctx	35.8
Control 4 Temporal Ctx	3.7	Control (Path) 2 Parietal Ctx	17.7
Control (Path) 1 Temporal Ctx	53.2	Control (Path) 3 Parietal Ctx	0.0
Control (Path) 2 Temporal Ctx	51.1	Control (Path) 4 Parietal Ctx	52.1

Table AVC. General_screening_panel_v1.4

Tissue Name	Rel. Exp.(%) Ag3349, Run 215620671	Tissue Name	Rel. Exp.(%) Ag3349, Run 215620671
Adipose	3.6	Renal ca. TK-10	1.9
Melanoma* Hs688(A).T	4.5	Bladder	35.4
Melanoma*		Gastric ca. (liver met.)	
Melanoma* LOXIMVI	0.5	Colon ca. SW-948	2.8

Melanoma* SK-MEL-5	8.0	Colon ca. SW480	10.2
Squamous cell carcinoma SCC-4	0.0	Colon ca.* (SW480 met) SW620	13.5
Testis Pool	5.4	Colon ca. HT29	0.0
Prostate ca.* (bone met) PC-3	0.8	Colon ca. HCT-116	0.7
Prostate Pool	15.1	Colon ca. CaCo-2	3.0
Placenta	0.0	Colon cancer tissue	7.0
Uterus Pool	0.4	Colon ca. SW1116	0.2
Ovarian ca. OVCAR-3	0.9	Colon ca. Colo-205	0.8
Ovarian ca. SK-OV-3	18.4	Colon ca. SW-48	0.0
Ovarian ca. OVCAR-4	0.0	Colon Pool	5.3
Ovarian ca. OVCAR-5	10.4	Small Intestine Pool	2.7
Ovarian ca. IGROV-1	0.3	Stomach Pool	5.8
Ovarian ca. OVCAR-8	1.3	Bone Marrow Pool	1.7
Ovary	5.0	Fetal Heart	2.0
Breast ca. MCF-7	1.0	Heart Pool	2.4
Breast ca. MDA-MB-231	1.3	Lymph Node Pool	8.9
Breast ca. BT 549	0.4	Fetal Skeletal Muscle	2.7
Breast ca. T47D	9.0	Skeletal Muscle Pool	0.0
Breast ca. MDA-N	1.6	Spleen Pool	0.4
Breast Pool	10.5	Thymus Pool	10.5
Trachea	1.2	CNS cancer (glio/astro) U87-MG	11.4
Lung	1.3	CNS cancer (glio/astro) U-118-MG	2.4
Fetal Lung	7.6	CNS cancer (neuro;met) SK-N-AS	0.1
Lung ca. NCI-N417	0.3	CNS cancer (astro) SF-539	0.2
Lung ca. LX-1	100.0	CNS cancer (astro) SNB-75	4.6
CNS cancer (astro) SF-539			
CNS cancer (astro) SNB-75			
Lung ca. A549	0.8	Brain (Amygdala) Pool	0.4

Lung ca. NCI-H526	0.0	Brain (cerebellum)	0.9
Lung ca. NCI-H23	7.1	Brain (fetal)	1.6
Lung ca. NCI-H460	0.8	Brain (Hippocampus) Pool	0.8
Lung ca. HOP-62	2.6	Cerebral Cortex Pool	2.3
Lung ca. NCI-H522	0.4	Brain (Substantia nigra) Pool	2.2
Liver	0.0	Brain (Thalamus) Pool	2.8
Fetal Liver	10.5	Brain (whole)	3.1
Liver ca. HepG2	0.8	Spinal Cord Pool	4.1
Kidney Pool	7.9	Adrenal Gland	2.4
Fetal Kidney	47.3	Pituitary gland Pool	1.4
Renal ca. 786-0	2.6	Salivary Gland	1.4
Renal ca. A498	0.9	Thyroid (female)	0.9
Renal ca. ACHN	1.3	Pancreatic ca. CAPAN2	3.7
Renal ca. UO-31	2.8	Pancreas Pool	9.3

Table AVD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3349, Run 165222879	Tissue Name	Rel. Exp.(%) Ag3349, Run 165222879
Secondary Th1 act	0.0	HUVEC IL-1beta	0.0
Secondary Th2 act	0.0	HUVEC IFN gamma	0.0
Secondary Tr1 act	0.8	HUVEC TNF alpha + IFN gamma	0.0
Secondary Th1 rest	0.0	HUVEC TNF alpha + IL4	0.0
Secondary Th2 rest	0.0	HUVEC IL-11	0.0
Secondary Tr1 rest	0.0	Lung Microvascular EC none	2.3
Primary Th1 act	0.0	Lung Microvascular EC TNFalpha + IL-1beta	0.0
Primary Th2 act	0.0	Microvascular Dermal EC none	2.3
Primary Tr1 act	0.0	Microvascular Dermal EC TNFalpha + IL-1beta	0.6
Primary Th1 rest	0.0	Bronchial epithelium TNFalpha + IL1beta	0.0
Primary Th2 rest	0.7	Small airway epithelium none	0.4
CD45RA CD4 lymphocyte act	0.0	Coronary artery SMC rest	0.0

CD45RO CD4 lymphocyte act	0.0	Coronary artery SMC TNFalpha + IL-1beta	0.0
CD8 lymphocyte act	0.0	Astrocytes rest	0.0
Secondary CD8 lymphocyte rest	0.0	Astrocytes TNFalpha + IL-1beta	1.0
Secondary CD8 lymphocyte act	0.0	KU-812 (Basophil) rest	0.0
CD4 lymphocyte none	0.0	KU-812 (Basophil) PMA/ionomycin	0.0
2ry Th1/Th2/Tr1_anti-CD95 CH11	0.0	CCD1106 (Keratinocytes) none	0.6
LAK cells rest	1.4	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	0.0
LAK cells IL-2	0.0	Liver cirrhosis	3.3
LAK cells IL-2+IL-12	0.0	Lupus kidney	5.8
LAK cells IL-2+IFN gamma	1.0	NCI-H292 none	0.6
LAK cells IL-2+ IL-18	0.0	NCI-H292 IL-4	0.0
LAK cells PMA/ionomycin	1.3	NCI-H292 IL-9	1.5
NK Cells IL-2 rest	0.0	NCI-H292 IL-13	0.8
Two Way MLR 3 day	0.0	NCI-H292 IFN gamma	0.3
Two Way MLR 5 day	0.0	HPAEC none	0.7
Two Way MLR 7 day	1.0	HPAEC TNF alpha + IL-1 beta	0.0
PBMC rest	0.0	Lung fibroblast none	0.0
PBMC PWM	0.0	Lung fibroblast TNF alpha + IL-1 beta	0.6
PBMC PHA-L	0.0	Lung fibroblast IL-4	0.0
Ramos (B cell) none	0.0	Lung fibroblast IL-9	0.9
Ramos (B cell) ionomycin	0.6	Lung fibroblast IL-13	0.0
B lymphocytes PWM	0.0	Lung fibroblast IFN gamma	0.0
B lymphocytes CD40L and IL-4	0.0	Dermal fibroblast CCD1070 rest	0.6
EOL-1 dbcAMP	0.0	Dermal fibroblast CCD1070 TNF alpha	0.8
EOL-1 dbcAMP PMA/ionomycin	0.0	Dermal fibroblast CCD1070 IL-1 beta	0.0
DENDRITIC CELLS			
Dendritic cells anti-CD40	2.9	IBD Colitis 2	0.0

Monocytes rest	0.0	IBD Crohn's	0.0
Monocytes LPS	1.3	Colon	0.6
Macrophages rest	0.9	Lung	0.7
Macrophages LPS	0.2	Thymus	100.0
HUVEC none	0.0	Kidney	1.7
HUVEC starved	0.0		

CNS_neurodegeneration_v1.0 Summary: Ag3349 This panel confirms the expression of CG57851-01 gene at low levels in the brains of an independent group of individuals. However, no differential expression of this gene was detected between Alzheimer's diseased postmortem brains and those of non-demented controls in this experiment. The expression of this gene in the brain suggests that therapeutic modulation of the expression or function of this gene may be useful in the treatment of neurologic disorders, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

General_screening_panel_v1.4 Summary: Ag3349 Highest expression of the CG57851-01 gene is seen in a lung cancer cell line (CT=30). Thus, expression of this gene may be used to differentiate between this sample and other samples on this panel and as a marker for lung cancer. This gene encodes a sulfotransferase homolog. Sulfotransferases are involved in the metabolism of drugs and endogenous compounds in the body and also synthesize the complex glycoproteins found on the cell surface of cancer cells. Therefore, therapeutic modulation of the expression or function of this gene may be effective in the treatment of lung cancer.

Among tissues with metabolic function, this gene is expressed at moderate to low levels in adipose and pancreas. This expression among these tissues suggests that this gene product may play a role in normal metabolic function and that dysregulated expression of this gene may contribute to metabolic diseases, such as obesity and diabetes.

Panel 4D Summary: Ag3349 Highest expression of the CG57851-01 gene is seen in the thymus (CT=29.7). The putative protein encoded by this gene could therefore play an important role in T cell development. Small molecule therapeutics designed against the protein encoded by this gene could be utilized to modulate immune function (T cell development) and be important for organ transplant, AIDS treatment or post chemotherapy immune

Panel 5 Islet Summary: Ag3349 Expression of the CG57851-01 gene is not detectable in all samples on this panel (CTs >35). (Data not shown.)

AW. CG59258-01: KIAA1608 protein

Expression of gene CG59258-01 was assessed using the primer-probe set Ag3520, described in Table AWA.

Table AWA. Probe Name Ag3520

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-cctcacagatgaggacacaga-3'	21	717	541
Probe	TET-5'-acttgcttgccaaagtcactcagcaa-3'- TAMRA	26	752	542
Reverse	5'-tttctgagagccagacagacat-3'	22	781	543

CNS_neurodegeneration_v1.0 Summary: Ag3520 Expression of the CG59258-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

General_screening_panel_v1.4 Summary: Ag3520 Expression of the CG59258-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

Panel 4D Summary: Ag3520 Expression of the CG59258-01 gene is low/undetectable in all samples on this panel (CTs>35). (Data not shown.)

AX. CG59564-01: Sorting nexin 6

Expression of gene CG59564-01 was assessed using the primer-probe set Ag3471, described in Table AXA. Results of the RTQ-PCR runs are shown in Tables AXB, AXC and AXD.

Table AXA. Probe Name Ag3471

Primers	Sequences	Length	Start Position	SEQ ID NO:
Forward	5'-gtgcctggcagacgattata-3'	20	820	544
Probe	TET-5'-ctatctcagctgcgctgagcagtcctg-3'- TAMRA	26	843	545
Reverse	5'-gtccttagctgggtgacttcct-3'	22	876	546

Tissue Name	Rel. Exp.(%) Ag3471, Run 210376963	Tissue Name	Rel. Exp.(%) Ag3471, Run 210376963
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AD 1 Hippo	10.8	Control (Path) 3 Temporal Ctx	2.4
AD 2 Hippo	27.0	Control (Path) 4 Temporal Ctx	28.5
AD 3 Hippo	5.9	AD 1 Occipital Ctx	10.3
AD 4 Hippo	10.8	AD 2 Occipital Ctx (Missing)	0.0
AD 5 Hippo	64.6	AD 3 Occipital Ctx	3.6
AD 6 Hippo	43.8	AD 4 Occipital Ctx	30.4
Control 2 Hippo	56.3	AD 5 Occipital Ctx	100.0
Control 4 Hippo	4.0	AD 6 Occipital Ctx	14.5
Control (Path) 3 Hippo	2.3	Control 1 Occipital Ctx	1.1
AD 1 Temporal Ctx	11.5	Control 2 Occipital Ctx	82.9
AD 2 Temporal Ctx	36.3	Control 3 Occipital Ctx	13.3
AD 3 Temporal Ctx	4.7	Control 4 Occipital Ctx	5.4
AD 4 Temporal Ctx	27.9	Control (Path) 1 Occipital Ctx	87.7
AD 5 Inf Temporal Ctx	85.9	Control (Path) 2 Occipital Ctx	10.3
AD 5 Sup Temporal Ctx	37.1	Control (Path) 3 Occipital Ctx	1.5
AD 6 Inf Temporal Ctx	46.3	Control (Path) 4 Occipital Ctx	12.2
AD 6 Sup Temporal Ctx	52.1	Control 1 Parietal Ctx	3.1
Control 1 Temporal Ctx	3.6	Control 2 Parietal Ctx	38.4
Control 2 Temporal Ctx	81.2	Control 3 Parietal Ctx	17.4
Control 3 Temporal Ctx	19.1	Control (Path) 1 Parietal Ctx	88.9
Control 3 Temporal Ctx	8.0	Control (Path) 2 Parietal Ctx	22.2
Control (Path) 1 Temporal Ctx	88.9	Control (Path) 3 Parietal Ctx	1.7
Control (Path) 2 Temporal Ctx	48.0	Control (Path) 4 Parietal Ctx	38.7

Tissue Name	Rel. Exp.(%) Ag3471,	Tissue Name	Rel. Exp.(%) Ag3471,
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	Run 222691297		Run 222691297
Adipose	2.3	Renal ca. TK-10	2.7
Melanoma* Hs688(A).T	3.1	Bladder	4.2
Melanoma* Hs688(B).T	4.2	Gastric ca. (liver met.) NCI-N87	6.3
Melanoma* M14	13.0	Gastric ca. KATO III	4.1
Melanoma* LOXIMVI	0.7	Colon ca. SW-948	0.7
Melanoma* SK- MEL-5	0.8	Colon ca. SW480	2.6
Squamous cell carcinoma SCC-4	1.5	Colon ca. * (SW480 met) SW620	4.5
Testis Pool	6.2	Colon ca. HT29	2.2
Prostate ca. * (bone met) PC-3	3.8	Colon ca. HCT-116	3.9
Prostate Pool	0.7	Colon ca. CaCo-2	3.5
Placenta	2.3	Colon cancer tissue	1.0
Uterus Pool	0.7	Colon ca. SW1116	1.9
Ovarian ca. OVCAR-3	5.3	Colon ca. Colo-205	0.6
Ovarian ca. SK-OV- 3	2.1	Colon ca. SW-48	2.3
Ovarian ca. OVCAR-4	2.8	Colon Pool	7.0
Ovarian ca. OVCAR-5	5.8	Small Intestine Pool	5.8
Ovarian ca. IGROV- 1	5.3	Stomach Pool	5.5
Ovarian ca. OVCAR-8	3.0	Bone Marrow Pool	3.5
Ovary	7.1	Fetal Heart	1.7
Breast ca. MCF-7	2.2	Heart Pool	3.1
Breast ca. MDA- MB-231	2.4	Lymph Node Pool	9.5
Breast ca. BT 549	98.6	Fetal Skeletal Muscle	1.4
Breast ca. T47D	8.4	Skeletal Muscle Pool	4.2
Breast ca. MDA-N	4.5	Spleen Pool	1.8
Breast Pool	7.5	Thymus Pool	6.2
Fetal Liver	2.7	CNS cancer (glio/astro)	7.0
Fetal Lung	13.4	CNS cancer	11.5

		(neuro;met) SK-N-AS	
Lung ca. NCI-N417	2.2	CNS cancer (astro) SF-539	1.9
Lung ca. LX-1	2.2	CNS cancer (astro) SNB-75	23.8
Lung ca. NCI-H146	2.1	CNS cancer (glio) SNB-19	3.6
Lung ca. SHP-77	3.7	CNS cancer (glio) SF-295	11.3
Lung ca. A549	3.7	Brain (Amygdala) Pool	22.1
Lung ca. NCI-H526	2.5	Brain (cerebellum)	42.9
Lung ca. NCI-H23	17.6	Brain (fetal)	100.0
Lung ca. NCI-H460	1.8	Brain (Hippocampus) Pool	26.6
Lung ca. HOP-62	3.6	Cerebral Cortex Pool	33.0
Lung ca. NCI-H522	5.7	Brain (Substantia nigra) Pool	29.3
Liver	0.1	Brain (Thalamus) Pool	37.4
Fetal Liver	1.3	Brain (whole)	55.1
Liver ca. HepG2	1.3	Spinal Cord Pool	7.7
Kidney Pool	10.6	Adrenal Gland	1.5
Fetal Kidney	6.7	Pituitary gland Pool	0.6
Renal ca. 786-0	0.9	Salivary Gland	0.8
Renal ca. A498	0.8	Thyroid (female)	0.8
Renal ca. ACHN	2.1	Pancreatic ca. CAPAN2	3.0
Renal ca. UO-31	3.4	Pancreas Pool	7.4

Table AXD. Panel 4D

Tissue Name	Rel. Exp.(%) Ag3471, Run 166417126	Tissue Name	Rel. Exp.(%) Ag3471, Run 166417126
Secondary Th1 act	10.2	HUVEC IL-1beta	2.3
Secondary Th2 act	11.2	HUVEC IFN gamma	7.8
Secondary Tr1 act	19.2	HUVEC TNF alpha + IFN gamma	4.7
Secondary Th1 rest	28.7	HUVEC TNF alpha + IL4	6.3
Secondary Th2 rest	18.4	HUVEC IL-11	6.2
Secondary Tr1 rest	24.5	Lung Microvascular EC none	6.4
Primary Th2 act	20.4	Microvascular Dermal EC none	6.9

Primary Tr1 act	31.0	Microvascular Dermal EC TNFalpha + IL-1beta	2.5
Primary Th1 rest	45.7	Bronchial epithelium TNFalpha + IL1beta	2.6
Primary Th2 rest	23.3	Small airway epithelium none	3.1
Primary Tr1 rest	25.3	Small airway epithelium TNFalpha + IL-1beta	3.3
CD45RA CD4 lymphocyte act	9.7	Coronary artery SMC rest	3.9
CD45RO CD4 lymphocyte act	23.2	Coronary artery SMC TNFalpha + IL-1beta	4.6
CD8 lymphocyte act	9.0	Astrocytes rest	12.7
Secondary CD8 lymphocyte rest	24.8	Astrocytes TNFalpha + IL-1beta	18.9
Secondary CD8 lymphocyte act	19.9	KU-812 (Basophil) rest	26.2
CD4 lymphocyte none	10.6	KU-812 (Basophil) PMA/ionomycin	50.0
2ry Th1/Th2/Tr1 _anti- CD95 CH11	22.7	CCD1106 (Keratinocytes) none	6.9
LAK cells rest	6.4	CCD1106 (Keratinocytes) TNFalpha + IL-1beta	10.9
LAK cells IL-2	27.5	Liver cirrhosis	15.3
LAK cells IL-2+IL-12	21.3	Lupus kidney	4.2
LAK cells IL-2+IFN gamma	27.4	NCI-H292 none	5.8
LAK cells IL-2+ IL-18	22.7	NCI-H292 IL-4	7.2
LAK cells PMA/ionomycin	8.2	NCI-H292 IL-9	3.6
NK Cells IL-2 rest	13.6	NCI-H292 IL-13	3.7
Two Way MLR 3 day	23.7	NCI-H292 IFN gamma	3.2
Two Way MLR 5 day	5.6	HPAEC none	3.7
Two Way MLR 7 day	7.7	HPAEC TNF alpha + IL-1 beta	2.3
PBMC rest	6.1	Lung fibroblast none	18.3
PBMC PWM	7.3	Lung fibroblast TNF alpha + IL-1 beta	20.6
PBMC PHA-L	7.1	Lung fibroblast IL-4	16.6
Ramos (B cell) none	6.3	Lung fibroblast IL-9	9.2
Ramos (B cell)			
B lymphocytes PWM		lung fibroblast IL-9 gamma	
B lymphocytes CD40L	11.1	Dermal fibroblast	11.4

and IL-4		CCD1070 rest	
EOL-1 dbcAMP	7.4	Dermal fibroblast CCD1070 TNF alpha	28.5
EOL-1 dbcAMP PMA/ionomycin	12.5	Dermal fibroblast CCD1070 IL-1 beta	7.2
Dendritic cells none	13.4	Dermal fibroblast IFN gamma	6.9
Dendritic cells LPS	14.0	Dermal fibroblast IL-4	12.8
Dendritic cells anti- CD40	15.9	IBD Colitis 2	1.7
Monocytes rest	21.3	IBD Crohn's	4.8
Monocytes LPS	11.4	Colon	100.0
Macrophages rest	23.5	Lung	12.6
Macrophages LPS	3.7	Thymus	8.9
HUVEC none	6.7	Kidney	34.4
HUVEC starved	11.0		

CNS_neurodegeneration_v1.0 Summary: Ag3471 This panel does not show differential expression of the CG59564-01 gene in Alzheimer's disease. However, this expression profile confirms the presence of this gene in the brain. Please see Panel 1.4 for discussion of utility of this gene in the central nervous system.

General_screening_panel_v1.4 Summary: Ag3471 The CG59564-01 gene, a sorting nexin homolog, shows highly brain preferential expression. Moderate levels of expression are seen in all brain regions examined, with highest expression in the fetal brain (CT=28.5). Thus, this gene would be useful for distinguishing brain tissue from non-neural tissue, and may be beneficial as a drug target in neurologic disease, such as Alzheimer's disease, Parkinson's disease, schizophrenia, multiple sclerosis, stroke and epilepsy.

Among tissues with metabolic function, this gene is expressed at low levels in pituitary, adipose, adrenal gland, pancreas, and adult and fetal skeletal muscle, heart, and liver. This widespread expression among these tissues suggests that this gene product may play a role in normal neuroendocrine and metabolic and that dysregulated expression of this gene may contribute to neuroendocrine disorders or metabolic diseases, such as obesity and diabetes.

In addition, this gene is expressed at significant levels in a breast cancer cell line

samples on this panel and as a marker for breast cancer